





241 HTSVCRSSCGLSNKENRLEENEMINLTIPHDKKSGPQVKLGSHKWYSFKKHRRYS 300  
 QY DR N-PSDB; AAT30433.  
 Db XX  
 Db PT Modifying feeding behaviour using Y5 receptor (ant) agonists - increases  
 PT or decreases food consumption, for treatment of e.g. obesity or bulimia.  
 Ps XX  
 Ps Claim 51; Fig 6; 23pp; English.

301 KKTACVLPAPEPSQENHSRILPENGSVRSLSSSSKFIPGVPTCPBIEKBENSVDHEL 360  
 Qy CC Human hippocampal Y5 receptor (AAR95939) was identified as the homologue  
 CC of rat hypothalamic Y5 receptor (AAR95940), isolated as an 'atypical Y1  
 CC receptor'. The receptor belongs to the G protein-coupled receptor  
 CC superfamily. It is encoded by a cDNA clone (see also RAT30433) that was  
 CC isolated from a hippocampus cDNA library using rat Y5 receptor cDNA as  
 CC probe. Recombinant rat Y5 receptor can be produced in prokarytic or  
 CC eukaryotic (e.g. COS-293 or SF9 insect) host cells. It is used to  
 CC identify Y5 ligands (agonists and antagonist) that can be used to treat  
 CC obesity, bulimia or anorexia, and to raise monoclonal antibodies useful  
 CC in detecting Y5 receptor  
 Db XX  
 Db Sequence 455 AA;

Qy Query Match 88.9%; Score 2326; DB 2*i*; Length 455;  
 Db Best Local Similarity 99.6%; Pred. No. 3.7e-229;  
 Db Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFYSKQDYNMIDLEDEYYNNTKLATEENNTAAATRNSDFPVWDDYKSSVDDLOXYFLIGLYTF 60  
 Db 1 MSFYSKQDYNMIDLEDEYYNNTKLATEENNTAAATRNSDFPVWDDYKSSVDDLOXYFLIGLYTF 60  
 Qy 61 VSLIIGPMGNLILIMALMKERNQKTTVNFLIGNLASDILVVLFCSPPLTTSVLLDDWMFG 120  
 Db 61 VSLIIGPMGNLILIMALMKERNQKTTVNFLIGNLASDILVVLFCSPPLTTSVLLDDWMFG 120  
 Qy 121 KVMCHIMPFLQCVSVLVSTLISIAIVRYHMKIPISSNLTAANTHCYFLIATWTLGFAI 180  
 Db 121 KVMCHIMPFLQCVSVLVSTLISIAIVRYHMKIPISSNLTAANTHCYFLIATWTLGFAI 180  
 Qy 181 CSPLPVFHSLVLEQETFGSALLSSRYLCVSWPSDSYRIATISILLYQYLPLVCLTVS 240  
 Db 181 CSPLPVFHSLVLEQETFGSALLSSRYLCVSWPSDSYRIATISILLYQYLPLVCLTVS 240  
 Qy 241 HTSVRSISCOLSNKENRLEENEMINLTIPHDKKSGPQVKLGSHKWYSFKKHRRYS 300  
 Db 241 HTSVRSISCOLSNKENRLEENEMINLTIPHDKKSGPQVKLGSHKWYSFKKHRRYS 300  
 Qy 301 KKTACVLPAPEPSQENHSRILPENGSVRSLSSSSKFIPGVPTCPBIEKBENSVDHEL 360  
 Db 301 KKTACVLPAPEPSQENHSRILPENGSVRSLSSSSKFIPGVPTCPBIEKBENSVDHEL 360  
 Qy 361 RVKRSVTRIKRSRSFVYRITLILYFASWMPFLHLFHVYTIDENQLNLSNRHFKVLYCIC 420  
 Db 361 RVKRSVTRIKRSRSFVYRITLILYFASWMPFLHLFHVYTIDENQLNLSNRHFKVLYCIC 420  
 Qy 421 HLLGMSCCLNPILYFLNNGIQRLI 446.  
 Db 421 HLLGMSCCLNPILYFLNNGIKADL 446

RESULT 4  
 ID AAW29447 standard; protein; 455 AA.  
 XX  
 AC AAW29447;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 26-FEB-1998 (first entry)

Human hippocampal neuropeptide Y Y5 receptor.  
 DE XX  
 KW Hippocampal; neuropeptide Y5 receptor; NPY Y5; antagonist;  
 KW epileptic seizure; migraine; sleep disturbance; prophylaxis;  
 KW eating disorder; quinazolin-2,4-diazirine.  
 XX OS Homo sapiens.

XX	PN	W09720822-A1.	Db	421 HLLGMMSCLNPILYGFNLNGIKADL	446
XX	PD	12-JUN-1997.	RESULT 5		
XX	PF	18-NOV-1996;	ID	AAW29413 standard; protein;	455 AA.
XX	PR	01-DEC-1995;	XX	AAW29413	
XX	PÄ	(NOVS ) NOVARTIS AG.	AC	AAW29413;	
XX	Rueeger H, Schmidlin T, Rigollier P, Yamaguchi Y;	XX	XX	XX	
PI	TintelnotBlomley M, Schilling W, Cricione L;	XX	XX	25-MAR-2003 (revised)	
XX	WPI; 1997-319712/29.	XX	XX	24-FEB-1998 (first entry)	
DR	N-PSDB; AAT89114.	XX	XX	XX	
XX	Use of new and known quinazolin-2,4-diazirine compounds as NPY Y5 receptor antagonists - for treating and preventing eating disorders, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, etc.	XX	XX	Human hippocampal neuropeptide Y Y5 receptor.	
PT	PT	XX	XX	KW	Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis; bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss; epileptic seizure; migraine; sleep disturbance; pain; depression; sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea; congestive heart failure; eating disorder; obesity.
PT	PT	XX	XX	DE	
PT	PT	XX	XX	XX	
PT	PT	XX	XX	XX	
PT	PT	XX	XX	XX	
XX	Disclosure; Page 127-129; 15pp; English.	XX	XX	XX	
PS	PS	XX	XX	XX	
XX	The present sequence represents human hippocampal neuropeptide (NPY) Y receptor subtype Y5, with a pharmacological function associated with, for example, obesity and eating disorders. The specification relates to a method of treatment and prophylaxis of disorders and diseases associated with NPY receptor subtype Y5 comprising administering to a warm-blooded animal, including man, in need of such treatment a therapeutically effective amount of a quinazolin-2,4-diazirine compound. These disorders and diseases include e.g. eating disorders, obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, pain, sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage, shock, congestive heart failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to correct PI field.)	XX	XX	XX	
XX	Sequence 455 AA;	XX	XX	XX	
Query	Match	Score 2326; DB 2; Length 455;	CC	This sequence represents human hippocampal neuropeptide (NPY) Y receptor subtype Y5, with a pharmacological function associated with, for example, obesity and eating disorders. The specification relates to a method of treatment and prophylaxis of disorders and diseases associated with NPY receptor subtype Y5 comprising administering to a warm-blooded animal, including man, in need of such treatment a therapeutically effective amount of a new heterocyclic compound. These disorders and diseases include e.g. eating disorders, obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, pain, sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage, shock, congestive heart failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to correct PI field.)	
Best Local Similarity	98.9%; Pred. No. 3	99.6%; Length 455;	CC		
Matches	44;	Conservative 1; Mismatches 1; Indels 0; Gaps 0;	CC		
Db	1	MSFYSKDYNMDLEDEYYNKTTLATEENNTAAATRNSDFPVWDDYKSSVDDOFLQYFLGIFTF	60		
Db	1	MSFYSKDYNMDLEDEYYNKTTLATEENNTAAATRNSDFPVWDDYKSSVDDOFLQYFLGIFTF	60		
Qy	61	VSLIGFMGNLILMALMKERNQKTTVNFELIGNLAFSDILYLVLPGSPFETITSVLLDNMGF	120		
Db	61	VSLIGFMGNLILMALMKERNQKTTVNFELIGNLAFSDILYLVLPGSPFETITSVLLDNMGF	120		
Db	61	KVMCHIMPLFQCVSVLTVSTLILISTAVYHMIKHPISNLNTANGYFELIATWTLGFAI	180		
Qy	121	KVMCHIMPLFQCVSVLTVSTLILISTAVYHMIKHPISNLNTANGYFELIATWTLGFAI	180		
Db	121	KVMCHIMPLFQCVSVLTVSTLILISTAVYHMIKHPISNLNTANGYFELIATWTLGFAI	180		
Qy	181	CSPLPVFHSLVEQTEFGSALLSSRYLCYESWPSDSYRAFTISLILYCYILPLVCLTVS	240		
Db	181	CSPLPVFHSLVEQTEFGSALLSSRYLCYESWPSDSYRAFTISLILYCYILPLVCLTVS	240		
Qy	241	HTSVCRSISCGLSKNSKENRLBENEMINLTLP SKGSQPKLSSHKWYSFIKKHRRYS	300		
Db	241	HTSVCRSISCGLSKNSKENRLBENEMINLTLP SKGSQPKLSSHKWYSFIKKHRRYS	300		
Qy	301	KKTCACVLPAPEPDSBNHSLPENFGSRSQLSSSKTIPGVPTCFFIKPEENSDVHEL	360		
Db	301	KKTCACVLPAPEPDSBNHSLPENFGSRSQLSSSKTIPGVPTCFFIKPEENSDVHEL	360		
Qy	361	RVKSRSVTRIKCRSRSSVYRTRILVLFAYSWMPHLFHVTDFNDNL1SNRHFKLVYCIC	420		
Db	361	RVKSRSVTRIKCRSRSSVYRTRILVLFAYSWMPHLFHVTDFNDNL1SNRHFKLVYCIC	420		
Qy	4221	HLLGMMSCLNPILYGFNLNGIKADL	446		





1 MSFYSKQDYNMDELDEYYNKTLATEENNTAAATRNSDFPWWDDYKSSVVDLQYFLIGLYTF 60  
 Qy 61 VSLLGFMGNLLILMALMKRNQKTTYNFLIGNLAFLSDILVYLFCSPFPLTSLVLDQWMFG 120  
 Db 61 VSLLGFMGNLLILMALMKRNQKTTYNFLIGNLAFLSDILVYLFCSPFPLTSLVLDQWMFG 120  
 Db 121 KWCCHIMPFLOQCVSVLSTLLISIAIVRYMIKHTSNNTANHGYFLATWTLGFAI 180  
 Qy 121 KWCCHIMPFLOQCVSVLSTLLISIAIVRYMIKHTSNNTANHGYFLATWTLGFAI 180  
 Db 121 KWCCHIMPFLOQCVSVLSTLLISIAIVRYMIKHTSNNTANHGYFLATWTLGFAI 180  
 Db 181 CSPLPYFHSLVLOEQTFGALLSSRYLCVESWPSDSYRAFTISLLVQYTLPLVCLTVS 240  
 Qy 181 CSPLPYFHSLVLOEQTFGALLSSRYLCVESWPSDSYRAFTISLLVQYTLPLVCLTVS 240  
 Db 241 HTSVCRSISCGLSNKENRLEENEMINLTLPISKSGFPQVKLGSHKWSYFTKGHRRYS 300  
 Qy 241 HTSVCRSISCGLSNKENRLEENEMINLTLPISKSGFPQVKLGSHKWSYFTKGHRRYS 300  
 Db 301 KKTACVLPAPEPQSQENHSRLIPENFGSRSOLSSSSKFITPGVPTCFEIKBEENSVDHBL 360  
 Qy 301 KKTACVLPAPEPQSQENHSRLIPENFGSRSOLSSSSKFITPGVPTCFEIKBEENSVDHBL 360  
 Db 301 KKTACVLPAPEPQSQENHSRLIPENFGSRSOLSSSSKFITPGVPTCFEIKBEENSVDHBL 360  
 Qy 361 RVKRSYTRIKRSRSVSYFRLTLLVLFVAWSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVKRSYTRIKRSRSVSYFRLTLLVLFVAWSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Qy 421 HLLGMNSCCLNPILYGFLLNGIQRLD 446  
 Db 421 HLLGMNSCCLNPILYGFLLNGIKADL 446

RESULT 9  
 ABBB4497 standard; protein; 455 AA.

XX ABBB4497;

XX DT 20-DEC-2002 (first entry)

XX BE Human hippocampus Y5 receptor protein.

XX Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor; food consumption; metabolic; anorectic; antidepressant; tranquiliser; antimigraine; analgesic; hypotensive; cerebroprotective; cardiant; antidiarrhoeic; haemostatic; vaccine; anorexia; obesity; bulimia; sexual disorder; reproductive disorder; depression; anxiety; memory loss; migraine; pain; epileptic seizure; hypertension; cerebral haemorrhage; shock; congestive heart failure; sleeve disturbance; nasal congestion; diarrhoea.

XX Homo sapiens.

XX PN US2002103123-A1.

XX PD 01-AUG-2002.

XX PF 24-SEP-2001; 2001US-00962646.

XX PR 02-DEC-1994; 94US-003494025.

XX PR 01-DEC-1995; 95US-00566196.

XX PR 25-NOV-1998; 98US-00200673.

XX PA (SYNA-) SYNAPTIC PHARM CORP.

XX PI Gerald CPG, Weinshank RL, Walker MW, Branchek T;

XX DR WPI: 2002-712388/77.

XX N-PSDB; AAF88821.

PT Modifying feeding behavior of subject, useful in treating feeding disorders, involves administering to subject Y5 receptor agonist or antagonist, to increase or decrease consumption of food by subject.

PS Claim 53; Fig 6; 102pp; English.  
 XX This invention describes a novel method of modifying feeding behaviour of a subject which involves administering to the subject an amount of a compound which is a Y5 receptor agonist or antagonist effective to increase or decrease, respectively, the consumption of food by the subject so as to modify feeding behaviour of the subject. The product of the invention has metabolic, anorectic, antidepressant, tranquiliser, antimigraine, analgesic, hypotensive, cerebroprotective, cardiant, antidiarrhoeic and haemostatic activity and can be used in a vaccine. Y5 receptor agonist or antagonist compounds are useful for treating a feeding disorder (e.g. anorexia, obesity or bulimia) in a subject. The pharmaceutical compositions described in the disclosure are useful for treating an abnormality alleviated by the inhibition or activation of Y5 receptor, in a subject. Antibodies raised against the receptor are useful for detecting the presence of the receptor on the surface of a cell. The agonist of Y5 receptor is useful for treating an abnormality in a subject, where the abnormality includes anorexia, sexual/reproductive disorder, depression, anxiety, memory loss, migraine, pain, epileptic seizure, hypertension, cerebral hemorrhage, shock, congestive heart failure, sleeve disturbance, nasal congestion, and diarrhoea. This sequence represents the human hippocampus Y5 receptor described in the disclosure of the invention  
 XX Sequence 455 AA;  
 SQ Sequence Match  
 Best Local Similarity 88.9%; Score 2326; DB 5; Length 455;  
 Matchers 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MSFYSKQDYNMDELDEYYNKTLATEENNTAAATRNSDFPWWDDYKSSVVDLQYFLIGLYTF 60  
 Db 1 MSFYSKQDYNMDELDEYYNKTLATEENNTAAATRNSDFPWWDDYKSSVVDLQYFLIGLYTF 60  
 Qy 61 VSLLGFMGNLLILMALMKRNQKTTYNFLIGNLAFLSDILVYLFCSPFPLTSLVLDQWMFG 120  
 Db 61 VSLLGFMGNLLILMALMKRNQKTTYNFLIGNLAFLSDILVYLFCSPFPLTSLVLDQWMFG 120  
 Db 121 KWCCHIMPFLOQCVSVLSTLLISIAIVRYMIKHTSNNTANHGYFLATWTLGFAI 180  
 Db 121 KWCCHIMPFLOQCVSVLSTLLISIAIVRYMIKHTSNNTANHGYFLATWTLGFAI 180  
 Db 181 CSPLPYFHSLVLOEQTFGALLSSRYLCVESWPSDSYRAFTISLLVQYTLPLVCLTVS 240  
 Qy 181 CSPLPYFHSLVLOEQTFGALLSSRYLCVESWPSDSYRAFTISLLVQYTLPLVCLTVS 240  
 Db 181 CSPLPYFHSLVLOEQTFGALLSSRYLCVESWPSDSYRAFTISLLVQYTLPLVCLTVS 240  
 Qy 241 HTSVCRSISCGLSNKENRLEENEMINLTLPISKSGFPQVKLGSHKWSYFTKGHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENRLEENEMINLTLPISKSGFPQVKLGSHKWSYFTKGHRRYS 300  
 Db 301 KKTACVLPAPEPQSQENHSRLIPENFGSRSOLSSSSKFITPGVPTCFEIKBEENSVDHBL 360  
 Qy 301 KKTACVLPAPEPQSQENHSRLIPENFGSRSOLSSSSKFITPGVPTCFEIKBEENSVDHBL 360  
 Db 301 KKTACVLPAPEPQSQENHSRLIPENFGSRSOLSSSSKFITPGVPTCFEIKBEENSVDHBL 360  
 Qy 361 RVKRSYTRIKRSRSVSYFRLTLLVLFVAWSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVKRSYTRIKRSRSVSYFRLTLLVLFVAWSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420  
 Qy 421 HLLGMNSCCLNPILYGFLLNGIQRLD 446  
 Db 421 HLLGMNSCCLNPILYGFLLNGIKADL 446

RESULT 10  
 ABB79510  
 ID ABB79510 standard; protein; 455 AA.  
 AC ABB79510;  
 DT 23-SEP-2002 (first entry)  
 XX Human hippocampus Y5 receptor protein.

XX Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor;

XX food consumption; metabolic; anorectic; antidepressant; tranquiliser;

XX antimigraine; analgesic; hypotensive; cerebroprotective; cardiant;

XX antidiarrhoeic; haemostatic; vaccine; anorexia; obesity; bulimia;

XX sexual disorder; reproductive disorder; depression; anxiety; memory loss;

XX migraine; pain; epileptic seizure; hypertension; cerebral haemorrhage;

XX shock; congestive heart failure; sleeve disturbance; nasal congestion;

XX diarrhoea.

OS Homo sapiens.

XX PN US2002103123-A1.

XX PD 01-AUG-2002.

XX PF 24-SEP-2001; 2001US-00962646.

XX PR 02-DEC-1994; 94US-003494025.

XX PR 01-DEC-1995; 95US-00566196.

XX PR 25-NOV-1998; 98US-00200673.

XX PA (SYNA-) SYNAPTIC PHARM CORP.

XX PI Gerald CPG, Weinshank RL, Walker MW, Branchek T;

XX DR WPI: 2002-712388/77.

XX N-PSDB; AAF88821.

PT Modifying feeding behavior of subject, useful in treating feeding

PT disorders, involves administering to subject Y5 receptor agonist or

PT antagonist, to increase or decrease consumption of food by subject.

XX Human neuropeptide Y5 receptor.

KW Neuropeptide Y5; NPY; NPY5; receptor; human; antagonist; anorectic;  
 KW antiinflammatory; nootropic; neuroprotective; human; antagonists; anorectic;  
 KW hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiovascular;  
 KW cerebroprotective; antidepressant; hæmostatic; tranquilizer;  
 KW neuroleptic; analgesic; antianginal; nephrotropic; uropathic;  
 KW gastrointestinal; antiasthmatic.  
 XX Homo sapiens.

PN WO200241152-A2.

XX PD -2002.

XX PR 11-DEC-2001; 2001WO-US047863.

XX PF 12-DEC-2000; 2000US-0254990P.

XX PA -) NEUROGEN CORP.

XX PI Bakthavatchalam R, Blum CA, Briellmann HL, Darrow JW, Elliott RL, Hammond M, Hutchison A, Tran J, Zheng X, XX

DR WPI; 2002-547845/58.

DR N-PSDB; ABN84252.

XX PT New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or 3H-spiroisobenzofuran-1,4'-piperidine, useful for treating, e.g. eating disorder, psychiatric, cardiovascular disorder or diabetes.

XX PT Example 675; Page 129-130; 134pp; English.

XX PS Sequence 455 AA;

XX CC The present sequence is the protein sequence for the human neuropeptide Y5 (NPY5) receptor. In an example from the invention, chimeric receptors including human NPY5 receptor sequences were constructed, and used to assay the binding activity of compounds of the invention. Substituted spiro(isobenzofuran-1,4'-piperidin)-3-ones and 3H-spiroisobenzofuran-1,4'-piperidines capable of modulating NPY5 receptor activity are provided.

CC Such compounds may be used to modulate ligand binding to NPY5 receptors in vivo or in vitro, and are particularly useful in the treatment of a variety of disorders, e.g. eating disorders such as obesity or bulimia, psychiatric disorders, diabetes and cardiovascular disorders such as hypertension, in humans and animals.

XX SQ Sequence 455 AA;

XX Query Match 88.9%; Score 2326; DB 5; Length 455;

XX Best Local Similarity 99.6%; Pred. No. 3.7e-229;

XX Matches 444; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFYSKQDNMDLDEYYNKTLATEENNTAATRNSDFPWDDYKSSVVDLQYFLIGYTF 60

Db 1 MSFYSKQDNMDLDEYYNKTLATEENNTAATRNSDFPWDDYKSSVVDLQYFLIGYTF 60

Qy 61 VSLIGFMGNILILMALKRNQKTTVNLIGNLAFTSDIIVLFCSPFTLTSVLDQNMFG 120

Db 61 VSLIGFMGNILILMALKRNQKTTVNLIGNLAFTSDIIVLFCSPFTLTSVLDQNMFG 120

Qy 121 KVMMCHIMPLIQCVCYLQVSTLISIAIVYHMKHPISNLTANHGTYLIAITWTLGFA 180

Db 121 KVMMCHIMPLIQCVCYLQVSTLISIAIVYHMKHPISNLTANHGTYLIAITWTLGFA 180

Qy 181 CSPLPVPHASLYLOETFGSALLSSRYLCTESWPSDSYRIAAFTISLLVQYILPLVCLTVS 240

Db 181 CSPLPVPHASLYLOETFGSALLSSRYLCTESWPSDSYRIAAFTISLLVQYILPLVCLTVS 240

Qy 241 HTSVCRSISGLSNKENRLEBENMINLTHPSKSGPOVQLSSHKWSYSPFKKHRRYS 300

Db 241 HTSVCRSISGLSNKENRLEBENMINLTHPSKSGPOVQLSSHKWSYSPFKKHRRYS 300

Qy 301 KKTAACVLPPAPERPSQENHSRILPENFGSTRSOLSSSKTFIPGVPTCFKXPEENSDVHEL 360

Db 301 KKTAACVLPPAPERPSQENHSRILPENFGSTRSOLSSSKTFIPGVPTCFKXPEENSDVHEL 360

Qy 361 RVKRSVTRIKKRSRSVVFYRLTILILPVAVSMPLHLFHWTENDNLISNRHKFLVYCIC 420

Db 361 RVKRSVTRIKKRSRSVVFYRLTILILPVAVSMPLHLFHWTENDNLISNRHKFLVYCIC 420

Qy 421 HLLGMMSCLNPILYGLNGIQL 446

Db 421 HLLGMMSCLNPILYGLNGIQL 446

RESULT 11

AA023266

ID AA023266 standard; protein; 455 AA.

XX

AC AA023266;

XX

DT 25-SEP-2003 (first entry)

XX

DE Human neuropeptide Y5 receptor (NPY5) protein.

XX

KW Neuropeptide Y5; receptor; NPY5; 2-cyclohexyl-4-phenyl-1H-imidazole; NPY;

KW appetite regulation; feeding disorder; obesity; bulimia; diabetes;

KW psychiatric; cardiovascular; hypertension; cerebral infarction; epilepsy;

KW schizophrenia; depression; angina; sudden cardiac death; vasospasm;

KW arrhythmia; urinary incontinence; Crohn's disease; asthma; neuroleptic;

KW antiinflammatory; nootropic; vasotropic; anticonvulsant; uropathic;

KW human.

XX Homo sapiens.

OS

PN EP1306085-A1.

XX

PD 02-MAY-2003.

XX

PP 21-OCT-2002; 2002EP-00023459.

XX

PR 23-OCT-2001; 2001US-0348974P.

XX

PA (NEUR-) NEUROGEN CORP.

XX

PI Blum CA, Briellmann HL, De Lombaert S, Zheng X;

XX

DR WPI; 2003-543553/52.

DR N-PSDB; AAL6583.

XX

PT New 2-cyclohexyl-4-phenyl-1H-imidazole derivatives are modulators of neuropeptide Y5 receptor activity, useful for treating e.g. eating or psychiatric disorders.

XX

PS Example 10; Page 39-41; 63pp; English.

XX

CC This invention relates to novel ligands (derivatives of 2-cyclohexyl-4-phenyl-1H-imidazole) for the neuropeptide Y5 (NPY5) receptor. The NPY5 receptor mediates a variety of physiological effects and is involved in appetite regulation, hormone release and blood pressure. Ligands that modulate the NPY5 receptor inhibit or enhance NPY binding such that they can be used to treat a variety of conditions including feeding disorders (obesity and bulimia), psychiatric disorders, diabetes and cardiovascular diseases such as hypertension. Further uses relate to the treatment of cerebral infarction, epilepsy, schizophrenia, depression, angina, sudden cardiac death, vasospasm, arrhythmia, urinary incontinence, Crohn's disease and asthma. As such these ligands can be described variously as neuroleptic, antiinflammatory, nootropic, vasotropic, anticonvulsant and uropathic. This polypeptide sequence is the human neuropeptide Y5 (NPY5) receptor protein of the invention

XX

SQ Sequence 455 AA;

XX

PT

Db	1 MSFYSKQDYNMDELDEYYNKTLENNTAAATRNSDFPVWDDYKSSVYDQYPLIGLYTF	60	DR WPI; 2004-390329/36.
Qy	61 VSLLGFMNLILMALMKRNOKTTYNFLIGNLAFLSDILVVLFCSPPTLTSVLLDWMFG	120	DR N-PSDB; ADO30001.
Db	61 VSLLGFMNLILMALMKRNOKTTYNFLIGNLAFLSDILVVLFCSPPTLTSVLLDWMFG	120	XX PT Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
Qy	121 KWCCHIMPFQCVSVLSTLILISIAIVRYMIKHPISNNUTANHGXYLIATWTLGFAI	180	PT PT PT XX
Db	121 KWCCHIMPFQCVSVLSTLILISIAIVRYMIKHPISNNUTANHGXYLIATWTLGFAI	180	PS XX
Db	121 KWCCHIMPFQCVSVLSTLILISIAIVRYMIKHPISNNUTANHGXYLIATWTLGFAI	180	XX
Qy	181 CSPLPVPHSYLVLQETPGSALLSSRYLCVESWPSDSYRIATFISLLVQYLPLVCLTVS	240	XX The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., arrhythmia or myocardial infarction); muscular disorders (e.g., blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.
Db	181 CSPLPVPHSYLVLQETPGSALLSSRYLCVESWPSDSYRIATFISLLVQYLPLVCLTVS	240	CC
Qy	241 HTSVCRSISCGLSUNKENRLEENEMINLTLPSSKSGPQVKLGSGHKWSYSTIKHRRYS	300	CC
Db	241 HTSVCRSISCGLSUNKENRLEENEMINLTLPSSKSGPQVKLGSGHKWSYSTIKHRRYS	300	CC
Qy	301 KKTACVLPPAPERPSQENHSRILIPENFGSVRSLSSSKFIFPGVPTCFEIKPBENSVDYHEL	360	CC
Db	301 KKTACVLPPAPERPSQENHSRILIPENFGSVRSLSSSKFIFPGVPTCFEIKPBENSVDYHEL	360	CC
Qy	361 RVKRSVTRIKERSRSVYRLTLLVFAVSMMPLHLFHVVTDFNDLISNRHFKLVYCIC	420	CC
Db	361 RVKRSVTRIKERSRSVYRLTLLVFAVSMMPLHLFHVVTDFNDLISNRHFKLVYCIC	420	CC
Qy	421 HLLGMNSCCLNPILYGPNNNGIKADL 4 46		CC
Db	421 HLLGMNSCCLNPILYGPNNNGIKADL 4 46		CC
<b>RESULT 12</b>			
ID	ADO29564 standard; protein: 455 AA.		CC
AC	ADO29564;		CC
XX			CC
DT	29-JUL-2004 (first entry)		CC
XX			CC
DB	Human GPCR NPYER, SEQ ID NO:666.		CC
KW	G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; anticancerian; antianamic; cytostatic; antiinflammatory; vasoconstrictor; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antilulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human; receptor.		CC
XX	Homo sapiens.		CC
PN	WO2004040000-A2.		CC
XX	13-MAY-2004.		CC
PP	09-SEP-2003; 2003WO-US028226.		CC
XX	09-SEP-2002; 2002US-0409203.		CC
PR	09-APR-2003; 2003US-0461329P.		CC
XX	(PRIM-) PRIMAL INC.		CC
PA	Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F; Madsen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;		CC
Qy	361 RVKRSVTRIKERSRSVYRLTLLVFAVSMMPLHLFHVVTDFNDLISNRHFKLVYCIC 420		CC

Db	361	RVERSVTRKCRSRSPVFRLLILVFAVSMPLHLFFVTDENDNLISNRHFKLVYCIC	420	Qy	121	KYCHIMPFQCVSVLVLSTLILISIAIVRYMIKHPISNNLTANHGFLIATWWTLGFAI	180
Qy	421	HLLGMMSCCLNPILYGLNNGIORDL	446	Db	121	KYCHIMPFQCVSVLVLSTLILISIAIVRYMIKHPISNNLTANHGFLIATWWTLGFAI	180
Db	421	HLLGMMSCCLNPILYGLNNGIADL	446	Qy	181	CSPLPVPHSLYVLOEQFGSALLSSRYLVEWPSDSYRAFTISLILVQYIPLVCUTVS	240
Db	421	HLLGMMSCCLNPILYGLNNGIADL	446	Db	181	CSPLPVPHSLYVLOEQFGSALLSSRYLVEWPSDSYRAFTISLILVQYIPLVCUTVS	240
RESULT 13							
AAE08016				Qy	241	HTSVCRSISCCGSNKENPBLNEEMINNTLHPSKSGPOVKLGSHKWMSYSFIKKHRRYRYS	300
ID AAE08016		standard protein; 455 AA.		Db	241	HTSVCRSISCCGSNKENPBLNEEMINNTLHPSKSGPOVKLGSHKWMSYSFIKKHRRYRYS	300
XX				Qy	301	KETACVLPAPERPSQNHRSRLPENFGSVRSLSSSSKFPQGVPTCFEIKPENSYTHEL	360
AC AAE08016;				Db	301	KETACVLPAPERPSQNHRSRLPENFGSVRSLSSSSKFPQGVPTCFEIKPENSYTHEL	360
XX				Db	361	RYKRSTRIGKRSRSVYRLTILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC	420
DT 01-NOV-2001		(first entry)		Qy	361	RYKRSTRIGKRSRSVYRLTILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC	420
XX	African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.			Db	361	RYKRSTRIGKRSRSVYRLTILVFAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC	420
DB				Qy	421	HLLGMMSCCLNPILYGLNNGIORDL	446
XX				Db	421	HLLGMMSCCLNPILYGLNNGIADL	446
Cercopithecus aethiops.							
XX				RESULT 14			
PN WO200155103-A2.				AAE08012			
XX				ID	AAE08012 standard, protein; 499 AA.		
PD 02-AUG-2001.				XX			
XX				AC	AAE08012;		
PF 29-JAN-2001; 2001WO-US002804.				XX			
XX				DT	01-NOV-2001 (first entry)		
PR 28-JAN-2000; 2000US-0178652P.				XX			
XX				DE	Rat chimeric rNPY5deltaRYCT receptor.		
PA (NEUR-) NEUROGEN CORP.				XX			
XX				KW	Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;		
Bennett M, Brodbeck R, Krause J;				KW	KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;		
XX				KW	KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;		
DRP1, 2001-514543/56.				KW	KW locomotor; anxiety disorder; tranquiliser; rat; tranquiliser; rat;		
DR N-PSDB; AAD14746.				KW	KW chimeric receptor.		
XX				OS	Rattus sp.		
New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development.				XX	WO200155103-A2.		
PT				XX			
PT				PD	02-AUG-2001.		
PS Example 2; Page 70-72; 72pp; English.				XX			
XX	The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY receptor may have an anti-epileptic control of limbic seizures. The present sequence is african green monkey (AGM) NPY5 receptor		PP 29-JAN-2001; 2001WO-US002804.				
SQ Sequence 455 AA;				XX	PR 28-JAN-2000; 2000US-0178652P.		
Query Match 88.6%; Score 2317; DB 4; Length 455;				XX	XX (NEUR-) NEUROGEN CORP.		
Best Local Similarity 99.1%; Pred. No. 3.1e-228; Mismatches 2; Indels 0; Gaps 0;				XX	Bennett M, Brodbeck R, Krause J;		
Matches 442; Conservative 2; Gaps 0;				XX	DRP1, 2001-514543/56.		
Qy 1 MSFYSKQDYNMDLEDDYNTKLATENNATRNSDFPWWDDYKGSVDDQFLIGLYTF 60				XX	XX New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development.		
Db 1 MSFYSKQDYNMDLEDDYNTKLATENNATRNSDFPWWDDYKGSVDDQFLIGLYTF 60				XX	XX Example 2; Page 64-65; 72pp; English.		
Qy 61 VSLJGFMGNLJLMLMKGKRNQKTTVNFLIGNLAISDNLAFSVDLVLFCSPPTITSVLUDQWMEG 120				XX	XX The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is rat chimeric		
Db 61 VSLJGFMGNLJLMLMKGKRNQKTTVNFLIGNLAISDNLAFSVDLVLFCSPPTITSVLUDQWMEG 120				XX	XX (NEUR-) NEUROGEN CORP.		

CC rNPY5deltaY1CT receptor. The chimera comprises C-terminal intracellular domain of NPY5 receptor replaced with C-terminal intracellular domain of NPY1 receptor

XX Sequence 499 AA:

Query Match 87.4%; Score 2285.5; DB 4; Length 499;  
Best Local Similarity 88.9%; Pred. No. 6.1e-225; Mismatches 30; Indels 3; Gaps 3;

Qy 7 QDYNMIDLEDEYYNKTLATEENNTAAATPNSDFPVWDDYKSYVDLQLFLIGLYTFVSLGF 66

Db 8 QDSSMWERKLEEFNPKTFPTENNTAAARNAAPAWEDYRGVSVDLQLFLIGLYTFVSLGF 67

Qy 67 MGNNLTIMALMKRKNQTKTYRNFLIGNAIFSDILVLFVLCSPPFITLTSVILDOWMEGKWMCHI 126

Db 68 MGNNLTIMAVMKRKNQTKTNFLIGNAIFSDILVLFVLCSPPFITLTSVILDQNMFGKAMCHI 127

Qy 127 MPFLQCVSVLVSTLLISIAIVRYMKHPISSNLTTANHGFLIATWTLGFAICSPLPV 186

Db 128 MPFLQCVSVLVSTLLISIAIVRYMKHPISSNLTTANHGFLIATWTLGFAICSPLPV 187

Qy 187 FHSVLVLEQTGSALLSSRYLCVSEWPSDSYRIATFISLLVQYLPLVCLTVSHTSVCR 246

Db 188 FHSVLVLEKTFSALLSSKYLCVSEWPSDSYRIATFISLLVQYLPLVCLTVSHTSVCR 247

Qy 247 SISCGLSNKENRLNEENMINLTLPSSKKSGPQVKLGSKHMWSYSFKKHKRRYRSKTTACV 306

Db 248 SISCGLSHKENRLNEENMINLTLPSSKSRSRNOAKTGSTQKSYSFSFRKHRRYRSKTTACV 307

Qy 307 LPAPERPSQENHSRILPENEGSVRSQISSLSSSKFPIGVPTCFBKEPBENSDVHELYVKRSV 366

Db 308 LPAPAGPSQGRHLAV-PENPAPSVRSQISSLSSKPIGVPTCFBKEPBENSDAHEMYVKRSI 366

Qy 367 TRIKKRSRSVPYRLLTLLVPAVSMPLHLPHVVTDFNDNLISNRHKFLVYCICHILGM 426

Db 367 TRIKKRSRSVPYRLLTLLVPAVSMPLHLPHVVTDFNDNLISNRHKFLVYCICHILGM 426

Qy 427 SCCLNPFLYGFUNNGI-QRDLOFFNFCDFRSRDDYETIAMSTMEHTDVSKTSKLKOASPV 485

Db 427 SCCLNPFLYGFUNNGIKORDLOFFNFCDFRSRDDYETIAMSTMEHTDVSKTSKLKOASPV 486

Qy 486 AFKKINNNDDNEKI 499

Db 487 AFKKISNN-DDNEKI 499

RESULT 15

AAE008010 ID AAE008010 standard; protein; 508 AA.

XX XX DT 01-NOV-2001 (first entry)

DE Mouse chimeric mNPY5deltaY1CT receptor.

XX KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;

KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;

KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;

KW locomotor; anxiety disorder; limbic seizure; tranquilliser; mouse;

XX KW chimeric receptor.

OS Mus sp.

XX PN WO20015103-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US002804.

XX PR 28-JAN-2000; 2000US-0178652P.

XX XX PA (NEUR-) NEUROGEN CORP.

XX PI Bennett M, Brodbeck R, Krause J;

XX DR WPI; 2001-514543/56.

XX PS Example 2; Page 61-62; 72pp; English.

XX CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.

CC PT The NPY receptors are G-protein-coupled transmembrane proteins with seven

CC PT amino acids, useful as targets for drug actions, and as basis for drug

CC PT discovery and development.

XX XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.

CC CC The NPY receptors are G-protein-coupled transmembrane proteins with seven

CC CC membrane spanning transmembrane (TM) domains. The compounds that modulate

CC CC the activity of NPY receptor is useful in the preparation of a

CC CC medicament for treating conditions including obesity, high/low blood

CC CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,

CC CC seizure, locomotor and anxiety disorders. They can also be used as

CC CC targets for drug actions, and as basis for drug discovery and

CC CC development. The NPY receptor may have an anti-spasmodic activity in the

CC CC control of limbic seizures. The present sequence is mouse chimeric

CC CC domain of NPY5 receptor replaced with C-terminal intracellular domain of

CC CC NPY1 receptor

XX SQ Sequence 508 AA:

Query Match 87.0%; Score 2276.5; DB 4; Length 508;

Best Local Similarity 85.9%; Pred. No. 5.2e-224;

Mismatches 24; Mismatches 25; Indels 23; Gaps 3;

Db 438; Conservative 24; Matched 438; Indels 23; Gaps 3;

Qy 11 MDLEDEYYNKTLATEENNTAA-

Db 1 MEVKDEBFNKTIVTENNTAA-SQNTASPAVEDYRGTEENNTSAARNIAFPFWEDYRSVDD 60

Qy 50 LQYFLIGLYTFVSLIGFMGNILILMALMKERNQKTTVNELJIGNLAIFSDILVLFCSFPTL 109

Db 61 LQYFLIGLYTFVSLIGFMGNILILNAVMKERNQKTTVNELJIGNLAIFSDILVLFCSFPTL 120

Qy 110 TSVLDQWMEGKVMCHIMPFLQCVSVLVTSLILISIAIVRYHMICKHPISNLTTANHGFL 169

Db 121 TSVLDQWMEGKAMCHIMPFLQCVSVLVTSLISIAIVRYHMICKHPISNLTTANHGFL 180

Qy 170 IATWVTLGFAICSPLPVFHSLVELQFTGSALLSSRLCYESWPSDSDYRAFTISLLVQ 229

Db 181 IATWVTLGFAICSPPFVHSVLVELQFTGSALLSSKYLCTESWPSDSDYRAFTISLLVQ 240

Qy 230 YILPLVCLTYSHTSTSRSISGLSNKERNLLEENEMINLTLPSSKSGPQVKLGGSHKWSY 289

Db 241 YILPLVCLTYSHTSTSRSISGLSNKERNLLEENEMINLTLPSSKSRDQAKPPSFRKWSY 300

AC 290 SPIKGHRRYSSKKTACVLPAPERPSQENHSRILPENFGSYRSQLOSSSSKTPGVPPTCPEI 349

DB 301 SFIRKGRYRSKKTACVLPAPAGPQQEKHLTV-PBNPGSYRSQLOSSSPSKVTPGVPPTCPEV 359

Qy 350 KPEENSDVHELRLVCKSVTRIKKRSRSVYFYRLLVFAVSWMPHLFHVVTDFDNLIS 409

Db 360 KPEEESSDAQEMRVKESLTRIKKRSRSVYFYRLLVFAVSWMPHLFHVVTDFDNLIS 419

Qy 410 NRHFPLVYCTICHLJGMSSCLNPILYGLPQNGIQDFFENFCDFRSRDDYETIAMST 469

Db 420 NRHFPLVYCTICHLJGMSSCLNPILYGLPQNGIQDFFENFCDFRSRDDYETIAMST 479

Qy 470 MHTDYSKTSLKQASPVAFKKINNNDDNEKI 499

Db 480 MHTDYSKTSLKQASPVAFKKISMN-DNEKV 508

Search completed: June 7, 2005, 17:55:39  
Job time : 167 secs



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OM protein - protein search, using sw model

Run on: June 7, 2005, 17:50:21 ; Search time 43 Seconds  
(without alignments)  
866,276 Million cell updates/sec

Title: US-09-771-956-9  
Perfect score: 2616  
Sequence: 1 MSFYSKQDYNMIDLEDDYNN.....KQASPVAFKKINNNDDNEKI 499

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/podata/1/iaa/5A\_COMB.pep:  
2: /cgn2\_6/podata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6/podata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6/podata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/podata/1/iaa/PCTUS\_COMB.pop:  
6: /cgn2\_6/podata/1/iaa/backfiles.pep:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2326	88.9	455	1	US-09-349-025-4	Sequence 4, Appli
2	2326	88.9	455	2	US-09-566-096A-4	Sequence 4, Appli
3	2326	88.9	455	3	US-09-668-650B-4	Sequence 4, Appli
4	2326	88.9	455	4	US-09-200-673-4	Sequence 4, Appli
5	2326	88.9	455	4	US-09-194-855-4	Sequence 4, Appli
6	2326	88.9	455	4	US-10-013-846-7	Sequence 7, Appli
7	2326	88.9	455	4	US-09-447-907-4	Sequence 4, Appli
8	2326	88.9	455	4	US-09-162-646-4	Sequence 4, Appli
9	2326	88.9	456	5	PCT-US5-15646-4	Sequence 4, Appli
10	2271	86.8	445	2	US-09-630-118A-6	Sequence 6, Appli
11	2271	86.8	445	2	US-09-138-399-6	Sequence 6, Appli
12	2271	86.8	445	2	US-09-003-199-21	Sequence 21, Appli
13	2271	86.8	445	3	US-09-235-939-6	Sequence 6, Appli
14	2271	86.8	445	3	US-09-127-035-6	Sequence 4, Appli
15	2271	86.8	445	4	US-09-065-027-2	Sequence 2, Appli
16	2271	86.8	445	4	US-09-708-192-13	Sequence 13, Appli
17	2267	86.7	445	4	US-09-165-077-4	Sequence 4, Appli
18	2262	86.5	445	3	US-09-040-958-4	Sequence 2, Appli
19	2262	86.5	445	3	US-09-040-958-4	Sequence 4, Appli
20	2262	86.5	445	4	US-09-126-519-533	Sequence 533, Appli
21	2212	84.6	456	4	US-08-668-650B-14	Sequence 14, Appli
22	2212	84.6	456	4	US-09-194-895-14	Sequence 14, Appli
23	2212	84.6	456	4	US-09-147-907-14	Sequence 14, Appli
24	2207	84.4	445	2	US-09-003-199-2	Sequence 2, Appli
25	2036.5	77.8	456	1	US-08-349-725-5	Sequence 2, Appli
26	2036.5	77.8	456	2	US-08-166-096A-2	Sequence 2, Appli
27	2036.5	77.8	456	2	US-08-668-650B-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-349-025-4  
; Sequence 4, Application US/08349025  
; Patent No. 5602024  
; GENERAL INFORMATION:  
; APPLICANT: Gerald, Christophe P.G.  
; APPLICANT: Walker, Mary W.  
; APPLICANT: Branchek, Theresa  
; APPLICANT: Weinshank, Richard L.  
; TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/349,025  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1795/46166  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0225  
; TELEX: 22233 COOP UU  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-349-025-4

Query Match 88 %; Score 2326; DB 1; Length 455;  
Best Local Similarity 99 %; Pred. No. 1.5e-168;  
Matches 444; Conservative 1; Mismatches 0; Gaps 0;  
Qy 1 MSFYSKQDYNMIDLEDDYNNKTLATEYNNKTLATRNSDFPWDDYKRSVDDIQLQYFLIGLYTF 60

US-08-566-096A-4

Db 1 MSFYSKQDYNMDLEDEYYNKTLENNTAAATRNSDFPVWDDYKSSVYDQLQYFLIGLYF 60  
 Qy 61 VSLIGFMENLITMALMKRNQKTTVNFLIGNIAFSDILUVVFCSPFELTSVLDQMF 120  
 Db 61 VSLIGFMNLITMALMKRNQKTTVNFLIGNIAFSDILUVVFCSPFELTSVLDQMF 120  
 Db 121 KYNCHIMPLCQVSYLVLISIATYRHMIKHPISNLTANHGYFLIATWTLGFA 180  
 Db 121 KYNCHIMPLCQVSYLVLISIATYRHMIKHPISNLTANHGYFLIATWTLGFA 180  
 Qy 181 CSPLPVFHSLVLOETFGSALLSSRYLCVEWPSDSYRAFTISLLIVQYILPLVCLTVS 240  
 Db 181 CSPLPVFHSLVLOETFGSALLSSRYLCVEWPSDSYRAFTISLLIVQYILPLVCLTVS 240  
 Qy 241 HTSVCRSISCGLSNKENLBEENMINLTHPSKSGPQVKLSSHKWSYSF1KKHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENLBEENMINLTHPSKSGPQVKLSSHKWSYSF1KKHRRYS 300  
 Qy 301 KKTAACVLPPAPERPSQENHSRILPENFGSVRSQLSSSSKEITPGYPTCFETIKPEENSDVHL 360  
 Db 301 KKTAACVLPPAPERPSQENHSRILPENFGSVRSQLSSSSKEITPGYPTCFETIKPEENSDVHL 360  
 Qy 361 RVGRSVTRIKRSRSVFEYLTLTLLVFAVSMPLHLFIVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVGRSVTRIKRSRSVFEYLTLTLLVFAVSMPLHLFIVTDFNDNLISNRHFKLVYCIC 420  
 Qy 421 HLLGMMSCCLNPILYGLFLNGIQDL 446  
 Db 421 HLLGMMSCCLNPILYGLFLNGIKADL 446

RESULT 2  
 US-08-566-096A-4  
 ; Sequence 4, Application US/08566096A  
 ; Patent No. 5968819  
 ; GENERAL INFORMATION  
 ; APPLICANT: Gerald, Christophe P.G.  
 ; APPLICANT: Walker, Mary W.  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Weinstank, Richard L.  
 ; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR,  
 ; COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC  
 ; NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/566,096A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 455 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: protein

US-08-566-096A-4

Query Match 98.9%; Score 2326; DB: 2; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-168;  
 Matches 444; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MSFYSKQDYNMDLEDEYYNKTLENNTAAATRNSDFPVWDDYKSSVYDQLQYFLIGLYF 60  
 Db 1 MSFYSKQDYNMDLEDEYYNKTLENNTAAATRNSDFPVWDDYKSSVYDQLQYFLIGLYF 60  
 Qy 61 VSLIGFMCNLITMALMKRNQKTTVNFLIGNIAFSDILUVVFCSPFELTSVLDQMF 120  
 Db 61 VSLIGFMCNLITMALMKRNQKTTVNFLIGNIAFSDILUVVFCSPFELTSVLDQMF 120  
 Qy 121 KYNCHIMPLCQVSYLVLISIATYRHMIKHPISNLTANHGYFLIATWTLGFA 180  
 Db 121 KYNCHIMPLCQVSYLVLISIATYRHMIKHPISNLTANHGYFLIATWTLGFA 180  
 Qy 181 CSPLPVFHSLVLOETFGSALLSSRYLCVEWPSDSYRAFTISLLIVQYILPLVCLTVS 240  
 Db 181 CSPLPVFHSLVLOETFGSALLSSRYLCVEWPSDSYRAFTISLLIVQYILPLVCLTVS 240  
 Qy 241 HTSVCRSISCGLSNKENLBEENMINLTHPSKSGPQVKLSSHKWSYSF1KKHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENLBEENMINLTHPSKSGPQVKLSSHKWSYSF1KKHRRYS 300  
 Qy 301 KKTAACVLPPAPERPSQENHSRILPENFGSVRSQLSSSSKEITPGYPTCFETIKPEENSDVHL 360  
 Db 301 KKTAACVLPPAPERPSQENHSRILPENFGSVRSQLSSSSKEITPGYPTCFETIKPEENSDVHL 360  
 Qy 361 RVGRSVTRIKRSRSVFEYLTLTLLVFAVSMPLHLFIVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RVGRSVTRIKRSRSVFEYLTLTLLVFAVSMPLHLFIVTDFNDNLISNRHFKLVYCIC 420  
 Qy 421 HLLGMMSCCLNPILYGLFLNGIQDL 446  
 Db 421 HLLGMMSCCLNPILYGLFLNGIKADL 446

RESULT 3  
 US-08-668-650B-4  
 ; Sequence 4, Application US/08668650B  
 ; Patent No. 5989320  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe P.G.  
 ; APPLICANT: Waker, Mary W.  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Weinstank, Richard L.  
 ; TITLE OF INVENTION: Methods of Modifying Feeding Behavior,  
 ; Compounds Useful In Such Methods, And DNA Encoding a  
 ; Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/668,650B  
 ; FILING DATE: 04-JUN-1996  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, Esg., John P.  
 ; REFERENCE/DOCKET NUMBER: 1795/46166-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 455 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: protein

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEX/FAX: 212-391-0525  
 INFORMATION FOR SEQ ID NO: 4 :  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-668-650B-4

Query Match 88.9%; Score 2326; DB 2; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-168;  
 Matches 444; Conservative 1; Mismatches 0; Gaps 0;  
 Query 1 MSFYSKQDYNMELDEYYNKTTLATEENNTAAATRNSDFPWDDYKSSVDDLQYFLGLYTF 60  
 Db 1 MSFYSKQDYNMELDEYYNKTTLATEENNTAAATRNSDFPWDDYKSSVDDLQYFLGLYTF 60  
 Query 1 VSLLGFMGNLILMALMKRNQKTTVNFLIGNLAESDLIVLFCSPFTLSVLLQWMMFG 120  
 Db 1 VSLLGFMGNLILMALMKRNQKTTVNFLIGNLAESDLIVLFCSPFTLSVLLQWMMFG 120  
 Query 1 KVMCHIMPFLQCVSVLVSTLILISIAIVRYMIKHPISSNLTANHGFYLIATWTLGFAI 180  
 Db 1 KVMCHIMPFLQCVSVLVSTLILISIAIVRYMIKHPISSNLTANHGFYLIATWTLGFAI 180  
 Query 1 VSLLGFMGNLILMALMKRNQKTTVNFLIGNLAESDLIVLFCSPFTLSVLLQWMMFG 120  
 Db 1 VSLLGFMGNLILMALMKRNQKTTVNFLIGNLAESDLIVLFCSPFTLSVLLQWMMFG 120  
 Query 1 CSPLPVFHSLVLEQTFGSALLSSRYLCVSWPSDSYRIASFATLSLIVQYFLPLVCLTVS 240  
 Db 1 CSPLPVFHSLVLEQTFGSALLSSRYLCVSWPSDSYRIASFATLSLIVQYFLPLVCLTVS 240  
 Query 1 KTMCHIMPFLQCVSVLVSTLILISIAIVRYMIKHPISSNLTANHGFYLIATWTLGFAI 180  
 Db 1 KTMCHIMPFLQCVSVLVSTLILISIAIVRYMIKHPISSNLTANHGFYLIATWTLGFAI 180  
 Query 1 CSPLPVFHSLVLEQTFGSALLSSRYLCVSWPSDSYRIASFATLSLIVQYFLPLVCLTVS 240  
 Db 1 CSPLPVFHSLVLEQTFGSALLSSRYLCVSWPSDSYRIASFATLSLIVQYFLPLVCLTVS 240  
 Query 1 HTSVCRSISCGLSNKENRLEEMINLTLSKSSPQVKLGSHKWSYSPIKKRRYS 300  
 Db 1 HTSVCRSISCGLSNKENRLEEMINLTLSKSSPQVKLGSHKWSYSPIKKRRYS 300  
 Query 1 HTSVCRSISCGLSNKENRLEEMINLTLSKSSPQVKLGSHKWSYSPIKKRRYS 300  
 Db 1 HTSVCRSISCGLSNKENRLEEMINLTLSKSSPQVKLGSHKWSYSPIKKRRYS 300  
 Query 1 KKTACVLPPAPERPSQENHSRLIPENFGSRQLPQVTCFEIKPEEENDSVHDL 446  
 Db 1 KKTACVLPPAPERPSQENHSRLIPENFGSRQLPQVTCFEIKPEEENDSVHDL 446  
 Query 1 KKTACVLPPAPERPSQENHSRLIPENFGSRQLPQVTCFEIKPEEENDSVHDL 360  
 Db 1 KKTACVLPPAPERPSQENHSRLIPENFGSRQLPQVTCFEIKPEEENDSVHDL 360  
 Query 1 RVKRSYTRIKRSRSYFYLRTILLYFAVSMPMLFLHVYTDENNLISRHFKLVYCIC 420  
 Db 1 RVKRSYTRIKRSRSYFYLRTILLYFAVSMPMLFLHVYTDENNLISRHFKLVYCIC 420  
 Query 1 RVKRSYTRIKRSRSYFYLRTILLYFAVSMPMLFLHVYTDENNLISRHFKLVYCIC 420  
 Db 1 RVKRSYTRIKRSRSYFYLRTILLYFAVSMPMLFLHVYTDENNLISRHFKLVYCIC 420  
 Query 1 HLLGMSCCLNPILGFLNNGIQRLD 446  
 Db 1 HLLGMSCCLNPILGFLNNGIKADL 446  
 Query 421 HLLGMSCCLNPILGFLNNGIQRLD 446  
 Db 421 HLLGMSCCLNPILGFLNNGIKADL 446

RESULT 5  
 US-09-194-895-4  
 ; Sequence 4, Application US/09194895  
 ; Patent No. 6531287  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe P.G.  
 ; APPLICANT: Weinhank, Richard L.  
 ; APPLICANT: Branchek, Therese  
 ; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful  
 ; in Such Methods, and DNA Encoding A Hypothalamic  
 ; Receptor (YS)  
 ; FILE REFERENCE: 1795-4616-D-PCT-US-JPW/BJA  
 ; CURRENT APPLICATION NUMBER: US/09/194,895  
 ; PRIORITY APPLICATION NUMBER: PCT/US97/09504  
 ; PRIORITY FILING DATE: 1998-09-27  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-194-895-4

Query Match 88.9%; Score 2326; DB 4; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-168;  
 Matches 444; Conservative 1; Mismatches 1; Gaps 0;  
 Query 1 MSFYSKQDYNMELDEYYNKTTLATEENNTAAATRNSDFPWDDYKSSVDDLQYFLGLYTF 60  
 Db 1 MSFYSKQDYNMELDEYYNKTTLATEENNTAAATRNSDFPWDDYKSSVDDLQYFLGLYTF 60  
 Query 1 VSLLGFMGNLILMALMKRNQKTTVNFLIGNLAESDLIVLFCSPFTLSVLLQWMMFG 120

Db 61 VSLIGFMNLILMALMKRNQKTTVNFIGNLAFSIDLVLFLCSPFPLTTSVLLDQMF 120  
 Qy 121 KVMCHIMPLQCVSVLTVSTLISIATVRYHMIKHPIISNNLTANHGFLIATWTLGFAI 180  
 Db 121 KVMCHIMPLQCVSVLTVSTLISIATVRYHMIKHPIISNNLTANHGFLIATWTLGFAI 180  
 Qy 181 CSPLPVFISLVEQETFSALLSRYLCVEWSPSDSYRAFTISLILVQYILPLVCLTVS 240  
 Db 181 CSPLPVFISLVEQETFSALLSRYLCVEWSPSDSYRAFTISLILVQYILPLVCLTVS 240  
 Qy 241 HTSVCRSISCGLSNKENRLEENMINLTLPSSKSGPQVKLGSHKWSYSFIKKHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENRLEENMINLTLPSSKSGPQVKLGSHKWSYSFIKKHRRYS 300  
 Qy 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360  
 Db 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360  
 Qy 361 RYKRSTRIKERSRSYFYRLTILIVFASWMPHLPHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RYKRSTRIKERSRSYFYRLTILIVFASWMPHLPHVVTDFNDNLISNRHFKLVYCIC 420  
 Qy 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360  
 Db 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360  
 Qy 421 HLGGMMSCLNPYLGFNINGIQLD 446  
 Db 421 HLGGMMSCLNPYLGFNINGIQLD 446  
 Db 361 RYKRSTRIKERSRSYFYRLTILIVFASWMPHLPHVVTDFNDNLISNRHFKLVYCIC 420  
 Db 361 RYKRSTRIKERSRSYFYRLTILIVFASWMPHLPHVVTDFNDNLISNRHFKLVYCIC 420  
 RESULT 7  
 US-09-447-907-4  
 ; Sequence 4; Application US/09447907  
 ; Patent No. 664574  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald, Christophe P. G.  
 ; APPLICANT: Weinhank, Richard L.  
 ; APPLICANT: Walker, Mary W.  
 ; APPLICANT: Branchek, Theresa  
 ; TITLE OF INVENTION: Methods of Modifying Feeding Behavior; Compounds Useful in Such Modification  
 ; FILE REFERENCE: 1795-4616CA  
 ; CURRENT APPLICATION NUMBER: US/09/447,907  
 ; PRIORITY APPLICATION NUMBER: 08/668,650  
 ; PRIOR FILING DATE: 1999-11-23  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Human Y5 cDNA clone  
 US-09-447-907-4

Query Match 88.9%; Score 2326; DB 4; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-168; Mismatches 1; Indels 0; Gaps 0;  
 Matches 444; Conservative 1;

Db 1 MSFYSKQDYNMDLDEYYNKTLATENTTAATNSDFPWWDDYKSVDNLDQYFLIGLYTF 60  
 Qy 1 MSFYSKQDYNMDLDEYYNKTLATENTTAATNSDFPWWDDYKSVDNLDQYFLIGLYTF 60  
 Db 1 MSFYSKQDYNMDLDEYYNKTLATENTTAATNSDFPWWDDYKSVDNLDQYFLIGLYTF 60  
 Qy 61 VSLIGFMNLILMALMKRNQKTTVNFIGNLAFSIDLVLFLCSPFPLTTSVLLDQMF 120  
 Db 61 VSLIGFMNLILMALMKRNQKTTVNFIGNLAFSIDLVLFLCSPFPLTTSVLLDQMF 120  
 Qy 121 KVMCIMPFLQCVSVLTVSTLISIATVRYHMIKHPIISNNLTANHGFLIATWTLGFAI 180  
 Db 121 KVMCIMPFLQCVSVLTVSTLISIATVRYHMIKHPIISNNLTANHGFLIATWTLGFAI 180  
 Qy 241 HTSVCRSISCGLSNKENRLEENMINLTLPSSKSGPQVKLGSHKWSYSFIKKHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENRLEENMINLTLPSSKSGPQVKLGSHKWSYSFIKKHRRYS 300  
 Qy 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360  
 Db 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360

RESULT 6  
 US-10-013-846-7  
 ; Sequence 7; Application US/10013846  
 ; Patent No. 6566167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bakhavatchalam, Rajagopal  
 ; APPLICANT: Blum, Charles A  
 ; APPLICANT: Brielman, Harry L  
 ; APPLICANT: Darow, James W  
 ; APPLICANT: De Lombert, Stephane  
 ; APPLICANT: Harchison, Alan  
 ; APPLICANT: Tran, Jennifer  
 ; APPLICANT: Zhang, Xiaozhang  
 ; APPLICANT: Elliott, Richard L  
 ; APPLICANT: Hammond, Marlys  
 ; TITLE OF INVENTION: Spiroisobenzofuran-1,4'-piperidin-3-one and  
 ; TITLE OF INVENTION: 3H-spirosobenzofuran-1,4'-piperidines  
 ; FILE REFERENCE: N00 2001  
 ; CURRENT FILING DATE: 2001-12-11  
 ; PRIOR APPLICATION NUMBER: US 60/254,990  
 ; PRIOR FILING DATE: 2000-12-12  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: homosapiens  
 US-10-013-846-7

Query Match 88.9%; Score 2326; DB 4; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-168; Mismatches 1; Indels 0; Gaps 0;  
 Matches 444; Conservative 1;

Db 1 MSFYSKQDYNMDLDEYYNKTLATENTTAATNSDFPWWDDYKSVDNLDQYFLIGLYTF 60  
 Qy 1 MSFYSKQDYNMDLDEYYNKTLATENTTAATNSDFPWWDDYKSVDNLDQYFLIGLYTF 60  
 Db 61 VSLIGFMNLILMALMKRNQKTTVNFIGNLAFSIDLVLFLCSPFPLTTSVLLDQMF 120  
 Qy 61 VSLIGFMNLILMALMKRNQKTTVNFIGNLAFSIDLVLFLCSPFPLTTSVLLDQMF 120  
 Db 61 VSLIGFMNLILMALMKRNQKTTVNFIGNLAFSIDLVLFLCSPFPLTTSVLLDQMF 120  
 Qy 121 KVMCIMPFLQCVSVLTVSTLISIATVRYHMIKHPIISNNLTANHGFLIATWTLGFAI 180  
 Db 121 KVMCIMPFLQCVSVLTVSTLISIATVRYHMIKHPIISNNLTANHGFLIATWTLGFAI 180  
 Qy 241 HTSVCRSISCGLSNKENRLEENMINLTLPSSKSGPQVKLGSHKWSYSFIKKHRRYS 300  
 Db 241 HTSVCRSISCGLSNKENRLEENMINLTLPSSKSGPQVKLGSHKWSYSFIKKHRRYS 300  
 Qy 301 KKTACVLPPAPERPSQENHSRLPENFSSRSOLSSSSKF1IPOVPTCEIKPEENSDYHEL 360

Db 301 KKTACVL PAPERPSQENHSRILPENFGSVRSQLSSSKFIPGVPTCEIKBPEENSDVHEL 360  
 Qy 361 RVKRSVTRIKRSRSVYRLTLLIVFAVSMPHLHFLHVVTDNDLISNRHFKLVYCIC 420  
 Db 361 RVKRSVTRIKRSRSVYRLTLLIVFAVSMPHLHFLHVVTDNDLISNRHFKLVYCIC 420  
 Qy 421 HLLGMMSCLNPLIGFLNNGIQDL 446  
 Db 421 HLLGMMSCLNPLIGFLNNGIQDL 446

---

**RESULT 8**  
 US-09-962-646-4  
 ; Sequence 4, Application US/09962646  
 ; Parent No. 6818445  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GERALD, CHRISTOPHE P.G.  
 ; APPLICANT: WEINSHANK, RICHARD L.  
 ; APPLICANT: WALKER, MARY W.  
 ; APPLICANT: BRANCHEK, THERESA  
 ; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND FILE REFERENCE: 1795/46166BA2  
 ; CURRENT FILING DATE: 2001-09-24  
 ; PRIOR APPLICATION NUMBER: US/09/962,646  
 ; PRIOR FILING DATE: 1998-11-25  
 ; PRIOR APPLICATION NUMBER: 08/566,096  
 ; PRIOR FILING DATE: 1995-12-01  
 ; PRIOR APPLICATION NUMBER: 08/349,025  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SEQ ID NO: 4  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-09-962-646-4

Query Match Score 2326; DB 4; Length 455;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-168;  
 Matches 444; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFYSKQDYNNDLEDEYYNKTLENNTAAATRNSDPPWDYKSSVDIQLQYFLIGLYTF 60  
 Db 1 MSFYSKQDYNNDLEDEYYNKTLENNTAAATRNSDPPWDYKSSVDIQLQYFLIGLYTF 60

Qy 61 VSLLGFMGNLILJLMALMKRNQKTTVNLIGNLAESDILVFLCSPPFTLSVLDQWMFG 120  
 Db 61 VSLLGFMGNLILJLMALMKRNQKTTVNLIGNLAESDILVFLCSPPFTLSVLDQWMFG 120  
 Db 61 VSLLGFMGNLILJLMALMKRNQKTTVNLIGNLAESDILVFLCSPPFTLSVLDQWMFG 120

Qy 121 KVMCHIMPFQCVSVLVLSTLILISIAIVRYHMIRKPIISNNLTANHGFLIATWTLGFLAI 180  
 Db 121 KVMCHIMPFQCVSVLVLSTLILISIAIVRYHMIRKPIISNNLTANHGFLIATWTLGFLAI 180

Qy 181 CSPLPVFHSLVQETFGSALLSSRYLCVSWPSDSYRAFTISLLVQVILPLVCLTVS 240  
 Db 181 CSPLPVFHSLVQETFGSALLSSRYLCVSWPSDSYRAFTISLLVQVILPLVCLTVS 240

Qy 241 HTSVCRSISCGSLNSKENRLEENMINLTHPSKSGPQVQLSGSHKWSFIKGHRRRYS 300  
 Db 241 HTSVCRSISCGSLNSKENRLEENMINLTHPSKSGPQVQLSGSHKWSFIKGHRRRYS 300

Qy 301 KKTACVL PAPERPSQENHSRILPENFGSVRSQLSSSKFIPGVPTCEIKBPEENSDVHEL 360  
 Db 301 KKTACVL PAPERPSQENHSRILPENFGSVRSQLSSSKFIPGVPTCEIKBPEENSDVHEL 360

Qy 361 RVKRSVTRIKRSRSVYRLTLLIVFAVSMPHLHFLHVVTDNDLISNRHFKLVYCIC 420  
 Db 361 RVKRSVTRIKRSRSVYRLTLLIVFAVSMPHLHFLHVVTDNDLISNRHFKLVYCIC 420

Qy 421 HLLGMMSCLNPLIGFLNNGIQDL 446

RESULT 10  
US 08-630-118A-6  
Sequence 6, Application US/08630118A  
Patent No. 5919301  
GENERAL INFORMATION  
APPLICANT: Hu Ph.D., Yinghe  
APPLICANT: Bloomquist Ph.D., Brian T.  
APPLICANT: Flores-Riveros Ph.D., Jaime R.  
APPLICANT: Cornfield Ph.D., Linda J.  
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, 32nd Floor  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,118A  
FILING DATE: April 8, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenfield Ph.D., Michael S.  
REGISTRATION NUMBER: 37,142  
REFERENCE/DOCKET NUMBER: 96,149/WH 405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)715-1000  
TELEFAX: (312)715-1234  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-118A-6

Query Match Score 2271; DB 2; Length 445;  
Best Local Similarity 99.5%; Pred. No. 2,2e-164;  
Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDLEDEYYNKTTLATENNTAAATRNSDFPDDYKSSVDSLQYFLIGLTFTVSLLGEMNL 70  
Db 1 MDLEDEYYNKTTLATENNTAAATRNSDFPDDYKSSVDSLQYFLIGLTFTVSLLGEMNL 60

Qy 71 LILMALMKERNQKTTVNFLIGLNLAFLSDTLYLFCSPFTLTSVLLDQMGKVMCHIMPL 130  
Db 61 LILMALMKERNQKTTVNFLIGLNLAFLSDTLYLFCSPFTLTSVLLDQMGKVMCHIMPL 120

Qy 131 QCYSVLVSTLISIAIVRYTHMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVEHSL 190  
Db 121 QCYSVLVSTLISIAIVRYTHMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVEHSL 180

Qy 191 VELQETFGSALLSSRYLCESWPSDSYRAFTISLLVQYLPLVCLTSHTSYCRS1SC 250  
Db 181 VELQETFGSALLSSRYLCESWPSDSYRAFTISLLVQYLPLVCLTSHTSYCRS1SC 240

Qy 251 GLSNKENRLEENEMINLTLPSSKGSPQYRLSGSHKWSYSFIKXHRRSKTACVL PAP 310

Db 241 GLSNKENRLEENEMINLTLPSSKGSPQYRLSGSHKWSYSFIKXHRRSKTACVL PAP 300

Qy 311 ERPSQENHSRILPENGSVRQSLSSSKFKIPGYPCTPEIKPENSYTHELVRKSRSTRIK 370  
Db 301 ERPSQENHSRILPENGSVRQSLSSSKFKIPGYPCTPEIKPENSYTHELVRKSRSTRIK 360

Qy 371 KRSRSVFYRLTILILVFAVSNMPLHLFRVTDNDLNUISNRHFKLVYCYCHLGMMSCL 430  
Db 361 KRSRSVFRLTILILVFAVSNMPLHLFRVTDNDLNUISNRHFKLVYCYCHLGMMSCL 420

RESULT 11  
US-08-638-399-6  
Sequence 6, Application US/08838399  
GENERAL INFORMATION  
PATENT NO. 5965192  
APPLICANT: Hu Ph.D., Yinghe  
APPLICANT: Bloomquist Ph.D., Michael L.  
APPLICANT: Flores-Riveros Ph.D., Jaime R.  
APPLICANT: Cornfield Ph.D., Linda J.  
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid  
TITLE OF INVENTION: Sequences  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,399  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Greenfield Ph.D., Michael S.  
REGISTRATION NUMBER: 37,147  
REFERENCE/DOCKET NUMBER: 96,149/WH 405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)715-1000  
TELEFAX: (312)715-1234  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-838-399-6

Query Match Score 2271; DB 2; Length 445;  
Best Local Similarity 99.5%; Pred. No. 2,2e-164;  
Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MDLEDEYYNKTTLATENNTAAATRNSDFPDDYKSSVDSLQYFLIGLTFTVSLLGEMNL 70  
Db 1 MDLEDEYYNKTTLATENNTAAATRNSDFPDDYKSSVDSLQYFLIGLTFTVSLLGEMNL 60

Qy 71 LILMALMKERNQKTTVNFLIGLNLAFLSDTLYLFCSPFTLTSVLLDQMGKVMCHIMPL 130  
Db 61 LILMALMKERNQKTTVNFLIGLNLAFLSDTLYLFCSPFTLTSVLLDQMGKVMCHIMPL 120

Qy 131 QCYSVLVSTLISIAIVRYTHMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVEHSL 190  
Db 121 QCYSVLVSTLISIAIVRYTHMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVEHSL 180

Qy 191 VELQETFGSALLSSRYLCESWPSDSYRAFTISLLVQYLPLVCLTSHTSYCRS1SC 250  
Db 181 VELQETFGSALLSSRYLCESWPSDSYRAFTISLLVQYLPLVCLTSHTSYCRS1SC 240

Qy 251 GLSNKENRLEENEMINLTLPSSKGSPQYRLSGSHKWSYSFIKXHRRSKTACVL PAP 310



MOLECULE TYPE: protein  
us-09-235-839-6

Query Match 86.8%; Score 2271; DB 3; Length 445;  
Best Local Similarity 99.5%; Pred. No. 2.e-16;  
Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MDLELDDEYNKTKLATEENNTAAATRNSDFPWDDYKSSVDDQFLIGHYTFSVLLGFMGNL 70  
Db 1 MDLELDDEYNKTKLATEENNTAAATRNSDFPWDDYKSSVDDQFLIGHYTFSVLLGFMGNL 60

Qy 71 LILMALKRKRNQKTTVNFLIGNIAFSDIIVLVLCSPTFTLTSVLLDQMGKWMCHIMPL 130  
Qy 61 LILMALKRKRNQKTTVNFLIGNIAFSDIIVLVLCSPTFTLTSVLLDQMGKWMCHIMPL 120

Db 131 QCVSVLVSTLISIAIVRYHMIKHPISNLNTANHGFLIATWTLGFAICSPLPVFHS 190  
Db 121 QCVSVLVSTLISIAIVRYHMIKHPISNLNTANHGFLIATWTLGFAICSPLPVFHS 180

Qy 191 VELOETFGSALLSSRYLCBSWPSDSYRAFTISLILLYQVYLPLVCLTYSHTSVCRSTSC 250  
Db 181 VELOETFGSALLSSRYLCBSWPSDSYRAFTISLILLYQVYLPLVCLTYSHTSVCRSTSC 240

Qy 251 GLSNKENRLEENEMINLTLPSSKSGPQKLSSSHKWSYSPFIKKHRRYSSKTFACVLPAP 310  
Db 241 GLSNKENRLEENEMINLTLPSSKSGPQKLSSSHKWSYSPFIKKHRRYSSKTFACVLPAP 300

Qy 311 ERPSQENHSRILPENFGSTRSOLSSSKTFEIKPEENSDVHLRVRSTRIK 370  
Db 301 ERPSQENHSRILPENFGSTRSOLSSSSKTFEIKPEENSDVHLRVRSTRIK 360

Qy 371 KRSRSVYFYRLTILLVFAVSWMPHLHFLHFTDNDNL1SNRHFKLVIC1CHLGMMSCL 430  
Db 361 KRSRSVYFYRLTILLVFAVSWMPHLHFLHFTDNDNL1SNRHFKLVIC1CHLGMMSCL 420

Qy 431 NPILYGFLLNGIQRL 446  
Db 421 NPILYGFLLNGIKADL 436

RESULT 14  
US -09-327-035-6

Correspondence Address:  
Sequence 6, Application US/09327035  
Addressee: McDonnell Boehnen Hulbert & Berghoff  
Street: 300 South Wacker Drive  
City: Chicago  
State: IL  
ZIP: 60606

Computer Readable Form:  
Computer: IBM PC compatible  
Medium Type: Floppy disk  
Operating System: PC-DOS/MS-DOS  
Software: PatentIn Release #1.0, Version #1.30

Current Application Data:  
Application Number: US/09/327,035  
Filing Date: 07-Jun-1999  
Classification: <Unknown>

Prior Application Data:  
Application Number: 08/838,399  
Filing Date: <Unknown>

Attorney/Agent Information:

NAME: Greenfield Ph.D., Michael S.  
REGISTRATION NUMBER: 37,147  
REFERENCE/DOCKET NUMBER: 96,149/WH 405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)715-1000  
TELEFAX: (312)715-1234  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-327-035-6

Query Match 86.8%; Score 2271; DB 3; Length 445;  
Best Local Similarity 99.5%; Pred. No. 2.e-16;  
Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MDLELDDEYNKTKLATEENNTAAATRNSDFPWDDYKSSVDDQFLIGHYTFSVLLGFMGNL 70  
Db 1 MDLELDDEYNKTKLATEENNTAAATRNSDFPWDDYKSSVDDQFLIGHYTFSVLLGFMGNL 60

Qy 71 LILMALKRKRNQKTTVNFLIGNIAFSDIIVLVLCSPTFTLTSVLLDQMGKWMCHIMPL 130  
Db 61 LILMALKRKRNQKTTVNFLIGNIAFSDIIVLVLCSPTFTLTSVLLDQMGKWMCHIMPL 120

Qy 131 QCVSVLVSTLISIAIVRYHMIKHPISNLNTANHGFLIATWTLGFAICSPLPVFHS 190  
Db 121 QCVSVLVSTLISIAIVRYHMIKHPISNLNTANHGFLIATWTLGFAICSPLPVFHS 180

Qy 71 LILMALKRKRNQKTTVNFLIGNIAFSDIIVLVLCSPTFTLTSVLLDQMGKWMCHIMPL 130  
Db 61 LILMALKRKRNQKTTVNFLIGNIAFSDIIVLVLCSPTFTLTSVLLDQMGKWMCHIMPL 120

Qy 131 QCVSVLVSTLISIAIVRYHMIKHPISNLNTANHGFLIATWTLGFAICSPLPVFHS 190  
Db 121 QCVSVLVSTLISIAIVRYHMIKHPISNLNTANHGFLIATWTLGFAICSPLPVFHS 180

Qy 191 VELOETFGSALLSSRYLCBSWPSDSYRAFTISLILLYQVYLPLVCLTYSHTSVCRSTSC 250  
Db 181 VELOETFGSALLSSRYLCBSWPSDSYRAFTISLILLYQVYLPLVCLTYSHTSVCRSTSC 240

Qy 251 GLSNKENRLEENEMINLTLPSSKSGPQKLSSSHKWSYSPFIKKHRRYSSKTFACVLPAP 310  
Db 241 GLSNKENRLEENEMINLTLPSSKSGPQKLSSSHKWSYSPFIKKHRRYSSKTFACVLPAP 300

Qy 311 ERPSQENHSRILPENFGSTRSOLSSSKTFEIKPEENSDVHLRVRSTRIK 370  
Db 301 ERPSQENHSRILPENFGSTRSOLSSSSKTFEIKPEENSDVHLRVRSTRIK 360

Qy 371 KRSRSVYFYRLTILLVFAVSWMPHLHFLHFTDNDNL1SNRHFKLVIC1CHLGMMSCL 430  
Db 361 KRSRSVYFYRLTILLVFAVSWMPHLHFLHFTDNDNL1SNRHFKLVIC1CHLGMMSCL 420

Qy 431 NPILYGFLLNGIQRL 446  
Db 421 NPILYGFLLNGIKADL 436

RESULT 15  
US-09-065-027-2

Sequence 2, Application US/09065027  
Patent No. 65283103

General Information:  
Applicant: Herzog, H.  
Title of Invention: NEUROPEPTIDE Y-Y5 RECEPTOR  
File Reference: 272402001800  
Current Application Number: US/09/065,027  
Prior Application Number: PCT/AU96/00706  
Prior Filing Date: 1996-11-08  
Number of SEQ ID NOS: 8  
Software: PatentIn Ver. 2.1  
SEQ ID NO 2  
Length: 445  
Type: PRT  
Organism: Homo sapiens  
US -09-065-027-2

Query Match 86.8%; Score 2271; DB 4; Length 445;

Best Local Similarity 99.5%; Pred. No. 2.2e-164;  
Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy	71	L I L M A L M K R N Q K T T I N F I G N L A F S D I L V V L F C S P P T L T S V I L L D O W M G K V M C H I M P F L
Db	61	L I L M A L M K R N Q K T T I N F I G N L A F S D I L V V L F C S P P T L T S V I L L D O W M G K V M C H I M P F L
Qy	131	Q C V S V I L V S T I L L I S I A I V R Y M I K H P I S S N I L T A N H G Y F L I A T W T I G F A I C S P L P V F H S L
Db	121	Q C V S V I L V S T I L L I S I A I V R Y M I K H P I S S N I L T A N H G Y F L I A T W T I G F A I C S P L P V F H S L
Qy	191	V E L Q E T F G S A L I S S R Y L C V E W P S D S Y R I A F T I S L I L V Q Y I L P L V C L T V S H T I V C R S I S C
Db	181	V E L Q E T F G S A L I S S R Y L C V E W P S D S Y R I A F T I S L I L V Q Y I L P L V C L T V S H T I V C R S I S C
Qy	251	G L S N K E N R L E E N E M I N I L I H P S K K G S P Q V K L S G H K W S Y S F I K K R Y S K K T A C V L P A P
Db	241	G L S N K E N R L E E N E M I N I L I H P S K K G S P Q V K L S G H K W S Y S F I K K R Y S K K T A C V L P A P
Qy	311	E R P S Q E N H S R I L P E N G S V R S Q L S S S K F I P G V P T C F E I K P E E N S D V H E L R V K R S V T R I K
Db	301	E R P S Q E N H S R I L P E N G S V R S Q L S S S K F I P G V P T C F E I K P E E N S D V H E L R V K R S V T R I K
Qy	371	K R S R S V F Y R I T I L L I V F A V S M P L H F H V Y T D F D N L I S N R H F K L V Y C I C H L G M M S C L
Db	361	K R S R S V F Y R I T I L L I V F A V S M P L H F H V Y T D F D N L I S N R H F K L V Y C I C H L G M M S C L
Qy	431	N P I L Y G F L I N N G I Q R D L 446
Db	421	N P I L Y G F L I N N G I K A D L 436

Search completed: June 7, 2005, 18:00:19  
Job time : 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 17:52:56 ; Search time 149 Seconds  
 (without alignments)  
 1206.318 Million cell updates/sec

Title: US-09-771-956-9

Perfect score: 2616

Sequence: 1 MSFYSKDYNMIDLEDEYNN... . . . . . KOASPVAFKINNNDDNEKI 499

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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 2: /cggn\_6/ptodata/1/pubpaas/US06\_PUB.dep: \*  
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 7: /cggn\_6/ptodata/1/pubpaas/US08\_NEWPUB.dep: \*  
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RESULT 1  
 US-09-771-956-9  
 ; Sequence 9, Application US/097711956  
 ; Patent No. US2001003144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, Michele  
 ; BROBECK, Robbie  
 ; ATTORNEY: Krause, James  
 ; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 ; FILE REFERENCE: N2000.001  
 ; CURRENT APPLICATION NUMBER: US/09/771,956  
 ; CURRENT FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 9  
 ; LENGTH: 499  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMMERA  
 US-09-771-956-9

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2616	100.0	499	9 US-09-771-956-9	Sequence 9, Appli
2	2326	88.9	455	9 US-09-771-956-13	Sequence 13, Appli
3	2326	88.9	455	9 US-09-962-646-4	Sequence 4, Appli
4	2326	88.9	455	14 US-10-013-946-7	Sequence 7, Appli
5	2326	88.9	455	15 US-10-410-948-7	Sequence 7, Appli
6	2317	88.6	455	9 US-09-771-956-30	Sequence 30, Appli
7	2309	88.3	455	14 US-10-274-851-7	Sequence 7, Appli
8	2285.5	87.4	499	9 US-09-771-956-24	Sequence 24, Appli
9	2276.5	87.0	508	9 US-09-771-956-22	Sequence 22, Appli
10	2271	86.8	445	14 US-10-027-949-6	Sequence 6, Appli
11	2271	86.8	445	14 US-10-225-967A-205	Sequence 205, Appli
12	2271	86.8	445	15 US-10-295-027-668	Sequence 668, Appli

Sequence 14, Appli  
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 Sequence 121, KVMCHIMPFLQCVSVLVLISSTLILISSIAIVRYHMKIPISNNLTANHGTYFLIATWTLGFAI 180



RESULT 4

Db 421 HLLGMMSCLNPILYGFLNNGIKADL 446

US-10-013-846-7

; Sequence 7, Application US/10013846

; Publication No. US20040072847A1

; GENERAL INFORMATION:

; APPLICANT: Bakthavatchalam, Rajagopal

; APPLICANT: Blum, Charles A.

; APPLICANT: Brielemann, Harry L.

; APPLICANT: Darrow, James W.

; APPLICANT: De Lombaert, Stephane W.

; APPLICANT: Hutchinson, Alan W.

; APPLICANT: Tran, Jennifer W.

; APPLICANT: Zheng, Xiaozhang W.

; APPLICANT: Elliott, Richard L.

; APPLICANT: Hammond, Marlys L.

; TITLE OF INVENTION: SPIROISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND 3H-SPIROISOBENZOFURAN-1,4'-PIPERIDINES

; FILE REFERENCE: U 014539-7

; CURRENT FILING DATE: 2003-04-09

; PRIORITY APPLICATION NUMBER: 10/013,846

; PRIORITY FILING DATE: 2001-12-11

; PRIORITY APPLICATION NUMBER: 60/254,990

; PRIORITY FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 7

; LENGTH: 455

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-410-648-7

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Query Match 88.9%; Score 2326; DB 14; Length 455;

Best Local Similarity 99.6%; Pred. No. 8.7e-190;

Matches 444; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MSFYSKQDYNNDLEDEYYNKTLATEENNTAAATRNSDFPWDDYKSSVDDIQLQFLIGLYTF 60

Db 1 MSFYSKQDYNNDLEDEYYNKTLATEENNTAAATRNSDFPWDDYKSSVDDIQLQFLIGLYTF 60

Qy 1 VSLLGFMGNLILJLMALMKRNQKTVNLIGLNLAESDILVLFCSPTLTSVLLQWMFG 120

Qy 1 VSLLGFMGNLILJLMALMKRNQKTVNLIGLNLAESDILVLFCSPTLTSVLLQWMFG 120

Db 61 VSLLGFMGNLILJLMALMKRNQKTVNLIGLNLAESDILVLFCSPTLTSVLLQWMFG 120

Db 61 VSLLGFMGNLILJLMALMKRNQKTVNLIGLNLAESDILVLFCSPTLTSVLLQWMFG 120

Qy 121 KVMCHIMPFLQCVSTVLVSTLISAVRYHMKPISNNLTANGYFLIATWTLGFAI 180

Db 121 KVMCHIMPFLQCVSTVLVSTLISAVRYHMKPISNNLTANGYFLIATWTLGFAI 180

Db 121 KVMCHIMPFLQCVSTVLVSTLISAVRYHMKPISNNLTANGYFLIATWTLGFAI 180

Qy 121 KVMCHIMPFLQCVSTVLVSTLISAVRYHMKPISNNLTANGYFLIATWTLGFAI 180

Db 121 KVMCHIMPFLQCVSTVLVSTLISAVRYHMKPISNNLTANGYFLIATWTLGFAI 180

Qy 181 CSPLPVFHSLVQETFGSALLSSRYLCV3SPDSYRAFTISLLLQVILPLVCLTVS 240

Db 181 CSPLPVFHSLVQETFGSALLSSRYLCV3SPDSYRAFTISLLLQVILPLVCLTVS 240

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Db 241 HTSVCRSISGCLSNENRLEENMINLTQPSKSGPQVLSGSKWSFSIKRRRRYS 300

Qy 301 KKTACVLPAPERPSQENHSRILPENFGSYRSQLOSSSSKFP1GVPCFEIKEPEENSDVHEL 360

Db 301 KKTACVLPAPERPSQENHSRILPENFGSYRSQLOSSSSKFP1GVPCFEIKEPEENSDVHEL 360

Qy 361 RVKRSVTRIKRSRSVPRYRITLILVFAYSWMPLHLFHVYTDFNDNLISNRHFKLVYCIC 420

Db 361 RVKRSVTRIKRSRSVPRYRITLILVFAYSWMPLHLFHVYTDFNDNLISNRHFKLVYCIC 420

Qy 421 HLLGMMSCLNPILYGFLNNGIKADL 446

Db 421 HLLGMMSCLNPILYGFLNNGIKADL 446

RESULT 6

US-09-771-956-30

; Sequence 5, Application US/09771956

; Publication No. US20040031474A1

; GENERAL INFORMATION:

; APPLICANT: Bennett, Michele

APPLICANT: Brodbeck, Robbin  
 APPLICANT: Krause, James  
 TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 FILE REFERENCE: N2000.001  
 CURRENT APPLICATION NUMBER: US/09/771,956  
 CURRENT FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 30  
 LENGTH: 455  
 TYPE: PRT  
 ORGANISM: Cercopithecus aethiops  
 US-09-771-956-30

Query Match 88.3%; Score 2309; DB 14; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 2, 4e-188;  
 Mismatches 1; Gaps 0;

Qy 1 MSFYSKQDNYMDLEDEYNKTLATEENNTAAATRNSDFPWDDYKSSVDDQYFLQYFLGTYF 60  
 Db 1 VSLIGFMGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFG 60  
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 Db 61 VSLIGFMGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFG 60  
 Qy 121 KVMCHIMPFQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI 180  
 Db 121 KVMCHIMPFQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI 180  
 Qy 121 KVMCHIMPFQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI 180  
 Db 121 KVMCHIMPFQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI 180  
 \* Query Match 88.6%; Score 2317; DB 9; Length 455;  
 Best Local Similarity 99.1%; Pred. No. 5.1e-189;  
 Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 MSFYSKQDNYMDLEDEYNKTLATEENNTAAATRNSDFPWDDYKSSVDDQYFLQYFLGTYF 60  
 Db 1 VSLIGFMGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFG 60  
 Qy 61 VSLIGFMGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFG 120  
 Db 61 VSLIGFMGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFG 120  
 Qy 121 KVMCHIMPFQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI 180  
 Db 121 KVMCHIMPFQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI 180  
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 Qy 181 CSPLPVFHSLVLEQFTGSAASSRLYCESWPDSYRAFTISLLVQYILPLVCLTVS 240  
 Db 181 CSPLPVFHSLVLEQFTGSAASSRLYCESWPDSYRAFTISLLVQYILPLVCLTVS 240  
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 Db 421 HLLGMMSCLNPFLYGLNINGIKADL 446

RESULT 8  
 US-09-771-956-24  
 Sequence 24, Application US/09771956  
 Patent No. US20010031474A1  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, Michelle  
 BRODBECK, Robbie  
 APPLICANT: Krause, James  
 TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 CURRENT APPLICATION NUMBER: N2000.001  
 CURRENT FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 24  
 LENGTH: 499  
 TYPE: PPT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA  
 US-09-771-956-24

RESULT 7  
 US-10-274-851-7  
 Sequence 7, Application US/10274851  
 Publication No. US20030144290A1  
 GENERAL INFORMATION:  
 APPLICANT: Blum, Charles  
 APPLICANT: Briellmann, Harry  
 APPLICANT: De Lombaert, Stephane  
 APPLICANT: Zheng, Xiaozhang  
 TITLE OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE DERIVATIVES  
 FILE REFERENCE: U 014209-8  
 CURRENT APPLICATION NUMBER: US/10/274,851  
 CURRENT FILING DATE: 2002-10-21  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 7  
 LENGTH: 455  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-274-851-7

Query Match 87.4%; Score 2285.5; DB 9; Length 499;  
 Best Local Similarity 88.9%; Pred. No. 2, 8e-186;  
 Mismatches 22; Gaps 3;

Qy 7 QDTMMDLEDEYNKTLATEENNTAAATRNSDFPWDDYKSSVDDQYFLQYFLGTYFVSLSLGF 66  
 Db 8 QDSMMEPFLLEHNPKTVTENNTAAARNAAFPAWEDQRGSVDPDQLQYFLQYFLGTYFVSLSLGF 67

Qy 67 MGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFGKVMCHI 126  
 Db 68 MGNLILMALMKRNQKTTVNFLIGNLAESDILVLFCSPEFTLSVLDQNMFGKAMCHI 127  
 Qy 127 MPFLQCVSVLVLILLISIAIVRYHMKHPISNNLTANHGFLIATWTLGPAI C8P0PV 186

Db 128 MPFLQCVSVLVLSTLILISIAIVYHMIKHPISNNLTANHGYFLIATWTLGFAICSPPLV 187  
 Qy 187 FHSVLVELQETFGSALLSSRYLCVEWNPDSYRSTRAFTTSLVLYQYILPVLCLTVSHTSVC 246  
 Db 188 FHSVLVELKETFSALLSSKYLCVESWSDSYRSTRAFTTSLVLYQYILPVLCLTVSHTSVC 247  
 Qy 247 STSGLSNKENLEENEMINLTLPSPSKRSGPQYKLGSNSYFSTKKHRRYSKCTACV 306  
 Db 248 STSGLSNKENLEENEMINLTLPSPSKRSGPQYKLGSNSYFSTKKHRRYSKCTACV 307  
 Qy 307 LPAPERSSQENHSRILPENFGSVRSQLSSSSKPIPGYPTCBEIKPEENSDVHELYKRSV 366  
 Db 308 LPAPAGSSQGHHLAV-PENPASVRSQULSPSSRSPSKVIGPVICPEVKPESSDAHEMRYKRSI 366  
 Qy 367 TRIKKRSRSVYFRTRTLLVFAVSWMPLHLFHVVTDEFNDNLJSNRHFKLVYCICHILGM 426  
 Db 367 TRIKKRSRSVYFRTRTLLVFAVSWMPLHLFHVVTDEFNDNLJSNRHFKLVYCICHILGM 426  
 RESULT 10-027-049-6  
 Qy 427 SCCLNPILYGFNLNGI-QRDLOFFNCDFRSRDDYETIAMSTMTHDVSCKTSLKQASPV 485  
 Db 427 SCCLNPILYGFNLNGI-KQRDLOFFNCDFRSRDDYETIAMSTMTHDVSCKTSLKQASPV 486  
 Qy 486 AFKKINNNDDNEKI 499  
 Db 487 AFKKISNN-DNEKI 499

RESULT 9  
 US-09-771-956-22  
 ; Sequence 22, Application US/09771956  
 ; Patent No. US20010031474A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, Michele  
 ; APPLICANT: Brodebeck, Robbin  
 ; APPLICANT: Krause, James  
 ; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors  
 ; FILE REFERENCE: N2000\_001  
 ; CURRENT APPLICATION NUMBER: US/09/771, 956  
 ; CURRENT FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO. 22  
 ; LENGTH: 508  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA  
 US-09-771-956-22

Query Match 87.0%; Score 2276.5; DB 9; Length 508;  
 Best Local Similarity 85.9%; Pred. No. 1.7e-185;  
 Matches 438; Conservative 24; Mismatches 25; Indels 23; Gaps 3;

Qy 11 MDLEDEYNYKTLENNTAAAT-----RNSDFPWYDDYKGSSVDD 49  
 Db 1 MEVKLBEEFKTFVTTNTAQSONTASPAWEDYRGTTNTSAARNTAPWMDYRGSSVDD 60  
 Qy 50 LQYFLGLYTYPSVSLIGMGNLILMAVKERNQKTYVNFLGNLAFSDLIVLFCSPFTL 109  
 Db 61 LQYFLGLYTYPSVSLIGMGNLILMAVKERNQKTYVNFLGNLAFSDLIVLFCSPFTL 120  
 ; US-10-027-049-6

Query Match 86.8%; Score 2271; DB 14; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4.2e-185;  
 Matches 434; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 111 TSVLQWMEGKVMCHIMPFQCVSVLVSPLLIISTIAIVYHMIKHPISNNLTANHGYFL 169  
 Db 121 TSVLQWMEGKVMCHIMPFQCVSVLVSPLLIISTIAIVYHMIKHPISNNLTANHGYFL 180  
 Qy 170 IATWTLGFAICSPPLVHSVLVQETFGSALLSSRYLCYESWPSDSYRAFTTSLVLUQ 229  
 Db 181 IATWTLGFAICSPPLVHSVLVQETFGSALLSSRYLCYESWPSDSYRAFTTSLVLUQ 240  
 Qy 230 YILPLVCLTVSHTSVCRSISCOLSNENMINTLHPSKKSGPQYKLGSNSHKWY 289  
 Db 241 YILPLVCLTVSHTSVCRSISCOLSNENMINTLHPSKKSRDQAQKPS1QKWSY 300  
 ; Db

290 SFIKHKRRYSKKTACTVLPAPERSSQENHSRILPENFGSVRSQLSSSSKFLPGVPPTCPEI 349  
 Db 301 SFTRKRRYRSKKTACTVLPAPGSPBKH1TV-PENPGS1RSQLSSSSKV1PGVP1CFEV 359  
 Qy 350 KPEENSDVHELYKRSVYTRIKRSRSVYRLLTLLVFAVSWMPLHFLHVVTDFNDNLIS 409  
 Db 360 KPEESSDAQEVKRSVLTTRIKRSRSVYRLLTLLVFAVSWMPLHFLHVVTDFNDNLIS 419  
 Qy 410 NRHFKLVYCICHILGMNSCCLNPILYGFNLNGIQRDLOFFNCDFRSRDDYETIAMST 469  
 Db 420 NRHFKLVYCICHILGMNSCCLNPILYGFNLNGIQRDQFPENFCDFRSRDDYETIAMST 479  
 Qy 470 MHTDVSXTS1KQASPYAFKK1NNNNDDNEKI 499  
 Db 480 MHTDVSXTS1KQASPYAFKK1SMN-DNEKV 508

RESULT 10-027-049-6  
 ; Sequence 6, Application US/10027049  
 ; Publication No. US20030022233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hu Ph.D., Yinghe  
 ; APPLICANT: McCaleb Ph.D., Michael L.  
 ; Bloomquist Ph.D., Brian T.  
 ; Flores-Riveros Ph.D., Jaime R.  
 ; Cornfield Ph.D., Linda J.  
 ; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid Sequences  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
 ; STREET: 300 South Wacker Drive, 32nd Floor  
 ; CITY: Chicago  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.1.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/027, 049  
 ; FILING DATE: 08-Apr-1996  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Greenfield Ph.D., Michael S.  
 ; REGISTRATION NUMBER: 37, 142  
 ; REFERENCE/DOCKET NUMBER: 96, 149/WH 405  
 ; TELEPHONE: (312)715-1000  
 ; TELEFAX: (312)715-1234  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: Protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 ; US-10-027-049-6

Qy 121 QCVSVLVLISLISIAIVRYMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVFHSI 190  
 Qy 121 QCVSVLVLISLISIAIVRYMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVFHSI 180  
 Db 121 QCVSVLVLISLISIAIVRYHMTRKHPISNNLTANHGYFLIATWTLGFAICSPLPVFHSI 180  
 Qy 191 VELQETFGALLSRYLCVESMPDSYRAFTISLLVQYLPLVCLTVSHTSVCRSISC 250  
 Qy 181 VELQETFGALLSRYLCVESMPDSYRAFTISLLVQYLPLVCLTVSHTSVCRSISC 240  
 Db 181 VELQETFGALLSRYLCVESMPDSYRAFTISLLVQYLPLVCLTVSHTSVCRSISC 240  
 Qy 251 GLSNKENRLEENEMINLTHPSKKSGLPQVKLSSSHKWSYSFIKKHRRYSKKTACTACVLPP 310  
 Db 241 GLSNKENRLEENEMINLTHPSKKSGLPQVKLSSSHKWSYSFIKKHRRYSKKTACTACVLPP 300  
 Qy 311 ERPSQENHSRILPENFGTSRQLSSSSKPTIPGVPTCFEKPKPEENSDVHLRVRSTRIK 370  
 Db 301 ERPSQENHSRILPENFGTSRQLSSSSKPTIPGVPTCFEKPKPEENSDVHLRVRSTRIK 360  
 Qy 371 KRSRSVFYRLTILLVFAVSWMPHLFHVTTDFNDNLISNRHFKLVYCCHLGMMSCL 430  
 Db 361 KRSRSVFYRLTILLVFAVSWMPHLFHVTTDFNDNLISNRHFKLVYCCHLGMMSCL 420  
 Qy 431 NPLYGFLNNGIQDL 446  
 Db 421 NPLYGFLNNGIKADL 436  
 Qy 311 ERPSQENHSRILPENFGTSRQLSSSSKPTIPGVPTCFEKPKPEENSDVHLRVRSTRIK 370  
 Db 301 ERPSQENHSRILPENFGTSRQLSSSSKPTIPGVPTCFEKPKPEENSDVHLRVRSTRIK 360  
 Qy 371 KRSRSVFYRLTILLVFAVSWMPHLFHVTTDFNDNLISNRHFKLVYCCHLGMMSCL 430  
 Db 361 KRSRSVFYRLTILLVFAVSWMPHLFHVTTDFNDNLISNRHFKLVYCCHLGMMSCL 420  
 Qy 431 NPLYGFLNNGIQDL 446  
 Db 421 NPLYGFLNNGIKADL 436  
 Qy 431 NPLYGFLNNGIQDL 446  
 Db 421 NPLYGFLNNGIKADL 436  
 RESULT 12 US-10-295-027-668  
 ; Sequence 668, Application US-10295027  
 ; Publication No. US20030232350A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alar, Daniel  
 ; APPLICANT: Ginzberg, Wendy M.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Glynn, Richard A.  
 ; APPLICANT: Hevez, Peter A.  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Watson, Susan R.  
 ; APPLICANT: BOS Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Cancer, Compositions and Screening for Modulators of Cancer  
 ; FILE REFERENCE: 018501-012500US  
 ; CURRENT APPLICATION NUMBER: US-10/295,027  
 ; CURRENT FILING DATE: 2002-11-13  
 ; PRIORITY NUMBER: US 09/663,733  
 ; PRIORITY FILING DATE: 2000-09-15  
 ; PRIORITY NUMBER: US 60/350,666  
 ; PRIORITY FILING DATE: 2001-11-13  
 ; PRIORITY NUMBER: US 60/335,394  
 ; PRIORITY FILING DATE: 2001-11-15  
 ; PRIORITY NUMBER: US 60/332,464  
 ; PRIORITY FILING DATE: 2001-11-21  
 ; PRIORITY NUMBER: US 60/334,393  
 ; PRIORITY FILING DATE: 2001-11-29  
 ; PRIORITY NUMBER: US 60/340,376  
 ; PRIORITY FILING DATE: 2001-12-14  
 ; PRIORITY NUMBER: US 60/347,211  
 ; PRIORITY FILING DATE: 2002-01-08  
 ; PRIORITY NUMBER: US 60/347,349  
 ; PRIORITY FILING DATE: 2002-01-10  
 ; PRIORITY NUMBER: US 60/355,250  
 ; PRIORITY FILING DATE: 2002-02-08  
 ; PRIORITY NUMBER: US 60/356,714  
 ; PRIORITY FILING DATE: 2002-02-13  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 205  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-225-567A-205  
 RESULT 11 US-10-225-567A-205  
 ; Sequence 205, Application US-10225567A  
 ; PRIORITY NUMBER: US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brown, Glenna C.  
 ; APPLICANT: Doush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 205  
 ; LENGTH: 445  
 ; Best Local Similarity 99.5%; Pred. No. 4 2e-185; Indels 0; Gaps 0;  
 ; Matches 434; Conservative 1; Mismatches 1;  
 ; MDLEDBYNKTLATEENNTAAATRNSDFFPWDDYKQSYVDIQLYFLIGLYTFVSLLGFMGNL 70  
 ; 1 MDLEDBYNKTLATEENNTAAATRNSDFFPWDDYKQSYVDIQLYFLIGLYTFVSLLGFMGNL 60  
 ; 1 MDLEDBYNKTLATEENNTAAATRNSDFFPWDDYKQSYVDIQLYFLIGLYTFVSLLGFMGNL 60  
 Query Match Score 2271; DB 14; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4 2e-185; Indels 0; Gaps 0;  
 Matches 434; Conservative 1; Mismatches 1;  
 Db 11 MDLEDBYNKTLATEENNTAAATRNSDFFPWDDYKQSYVDIQLYFLIGLYTFVSLLGFMGNL 70  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-295-027-668  
 Query Match Score 2271; DB 15; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4 2e-185; Indels 0; Gaps 0;  
 Matches 434; Conservative 1; Mismatches 1;  
 Db 11 MDLEDBYNKTLATEENNTAAATRNSDFFPWDDYKQSYVDIQLYFLIGLYTFVSLLGFMGNL 70  
 ; 1 MDLEDBYNKTLATEENNTAAATRNSDFFPWDDYKQSYVDIQLYFLIGLYTFVSLLGFMGNL 60  
 Qy 71 LILMALMKRNQKTTTFLIGNLAFLSPLVYQYLPLVCLTVSHTSVCRSISC 250  
 Db 61 LILMALMKRNQKTTTFLIGNLAFLSPLVYQYLPLVCLTVSHTSVCRSISC 240  
 Qy 131 QCVSVLVLISLISIAIVRYMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVFHSI 190  
 Db 121 QCVSVLVLISLISIAIVRYMIKHPISNNLTANHGYFLIATWTLGFAICSPLPVFHSI 180  
 Qy 191 VELQETFGALLSRYLCVESMPDSYRAFTISLLVQYLPLVCLTVSHTSVCRSISC 250  
 Db 181 VELQETFGALLSRYLCVESMPDSYRAFTISLLVQYLPLVCLTVSHTSVCRSISC 240  
 Qy 251 GLSNKENRLEENEMINLTHPSKSKGPVKLSSSHKWSYSFIKKHRRYSKKTACTACVLPP 310  
 Db 241 GLSNKENRLEENEMINLTHPSKSKGPVKLSSSHKWSYSFIKKHRRYSKKTACTACVLPP 300  
 Qy 71 LILMALMKRNQKTTTFLIGNLAFLSPLVYQYLPLVCLTVSHTSVCRSISC 250  
 Db 61 LILMALMKRNQKTTTFLIGNLAFLSPLVYQYLPLVCLTVSHTSVCRSISC 240

Qy 131 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 190  
 Db 121 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 180  
 Qy 191 VBLQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 250  
 Db 181 VBLQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 240  
 Qy 251 GLSNKENRLEENEMINLTBPKKSQVQLGSHKWMSYSFIKKHRRYSKTKTACVLPP 310  
 Db 241 GLSNKENRLEENEMINLTBPKKSQVQLGSHKWMSYSFIKKHRRYSKTKTACVLPP 300  
 Qy 311 ERPSQENHSRILPENFGSVRSQLSSSSKFPIPGVPCTFEIKPEENSDVHLRKRSYTRIK 370  
 Db 301 ERPSQENHSRILPENFGSVRSQLSSSSKFPIPGVPCTFEIKPEENSDVHLRKRSYTRIK 360  
 Qy 371 KRSRSVYRFLTLLVLYAVSMPMLHFHVVTDFNDLNSRHFKLYCICHLLGMNSCL 430  
 Db 361 KRSRSVYRFLTLLVLYAVSMPMLHFHVVTDFNDLNSRHFKLYCICHLLGMNSCL 420  
 Qy 431 NPILGFNLNGIORDL 446  
 Db 421 NPILGFNLNGIADL 436

RESULT 14  
 US-10-686-390-13  
 ; Sequence 13, Application US/10686390  
 ; Publication No. US20040254153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pfizer Inc.  
 ; ATTORNEY OR AGENT: Maw, Graham Nigel  
 ; APPLICANT: Wayman, Christopher Peter  
 ; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction  
 ; FILE REFERENCE: PC1043B  
 ; CURRENT APPLICATION NUMBER: US/10/686,390  
 ; CURRENT FILING DATE: 2003-10-15  
 ; PRIOR APPLICATION NUMBER: US 09/708,392  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/175,161  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: GB 9926437.6  
 ; PRIOR FILING DATE: 1999-11-08  
 ; PRIOR APPLICATION NUMBER: GB 0004021.2  
 ; PRIOR FILING DATE: 2000-02-18  
 ; PRIOR APPLICATION NUMBER: GB 0013001.3  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 0016563.9  
 ; PRIOR FILING DATE: 2000-07-05  
 ; PRIOR APPLICATION NUMBER: GB 0017141.3  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/192,962  
 ; PRIOR FILING DATE: 2000-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/217,479  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: US 60/221,014  
 ; PRIOR FILING DATE: 2000-07-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 13  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-181-906-14

Query Match 86.8%; Score 2271; DB 15; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4.2e-185;  
 Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDLELDDEYNYKNTLATEENNTAAATRNSDPWDYKSEVDIQLQYFLIGLYTFSLLGFMGNL 70  
 Db 1 MDLELDDEYNYKNTLATEENNTAAATRNSDPWDYKSEVDIQLQYFLIGLYTFSLLGFMGNL 60

Query Match 86.8%; Score 2271; DB 16; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4.2e-185;  
 Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 71 LILMAIMKRNQKTTVNFLGNLAFDILVLFCSPTLTSVLLQWMGKVMCHIMPFL 130  
 Db 61 LILMAIMKRNQKTTVNFLGNLAFDILVLFCSPTLTSVLLQWMGKVMCHIMPFL 120

Qy 131 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 190  
 Db 121 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 180  
 Qy 191 VELQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 250  
 Db 181 VELQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 240  
 Qy 251 GLSNKENRLEENEMINLTBPKKSQVQLGSHKWMSYSFIKKHRRYSKTKTACVLPP 310  
 Db 241 GLSNKENRLEENEMINLTBPKKSQVQLGSHKWMSYSFIKKHRRYSKTKTACVLPP 300

Qy 311 ERPSQENHSRILPENFGSVRSQLSSSSKFPIPGVPCTFEIKPEENSDVHLRKRSYTRIK 370  
 Db 301 ERPSQENHSRILPENFGSVRSQLSSSSKFPIPGVPCTFEIKPEENSDVHLRKRSYTRIK 360  
 Qy 371 KRSRSVYRFLTLLVLYAVSMPMLHFHVVTDFNDLNSRHFKLYCICHLLGMNSCL 430  
 Db 361 KRSRSVYRFLTLLVLYAVSMPMLHFHVVTDFNDLNSRHFKLYCICHLLGMNSCL 420  
 Qy 431 NPILGFNLNGIORDL 446  
 Db 421 NPILGFNLNGIADL 436

RESULT 15  
 US-10-686-390-15  
 ; Sequence 15, Application US/10686390  
 ; Publication No. US20040254153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pfizer Limited  
 ; ATTORNEY OR AGENT: Maw, Graham Nigel  
 ; APPLICANT: Wayman, Christopher Peter  
 ; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction  
 ; FILE REFERENCE: PC1043B  
 ; CURRENT APPLICATION NUMBER: US/10/686,390  
 ; CURRENT FILING DATE: 2003-10-15  
 ; PRIOR APPLICATION NUMBER: US 09/708,392  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/175,161  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: GB 9926437.6  
 ; PRIOR FILING DATE: 1999-11-08  
 ; PRIOR APPLICATION NUMBER: GB 0004021.2  
 ; PRIOR FILING DATE: 2000-02-18  
 ; PRIOR APPLICATION NUMBER: GB 0013001.3  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 0016563.9  
 ; PRIOR FILING DATE: 2000-07-05  
 ; PRIOR APPLICATION NUMBER: GB 0017141.3  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/192,962  
 ; PRIOR FILING DATE: 2000-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/217,479  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: US 60/221,014  
 ; PRIOR FILING DATE: 2000-07-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 13  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-686-390-13

Query Match 86.8%; Score 2271; DB 16; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4.2e-185;  
 Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MDLELDDEYNYKNTLATEENNTAAATRNSDPWDYKSEVDIQLQYFLIGLYTFSLLGFMGNL 70  
 Db 1 MDLELDDEYNYKNTLATEENNTAAATRNSDPWDYKSEVDIQLQYFLIGLYTFSLLGFMGNL 60

Query Match 86.8%; Score 2271; DB 17; Length 445;  
 Best Local Similarity 99.5%; Pred. No. 4.2e-185;  
 Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 71 LILMAIMKRNQKTTVNFLGNLAFDILVLFCSPTLTSVLLQWMGKVMCHIMPFL 130  
 Db 61 LILMAIMKRNQKTTVNFLGNLAFDILVLFCSPTLTSVLLQWMGKVMCHIMPFL 120

Qy 131 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 190  
 Db 121 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 180  
 Qy 191 VELQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 250  
 Db 181 VELQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 240  
 Qy 251 GLSNKENRLEENEMINLTBPKKSQVQLGSHKWMSYSFIKKHRRYSKTKTACVLPP 310  
 Db 241 GLSNKENRLEENEMINLTBPKKSQVQLGSHKWMSYSFIKKHRRYSKTKTACVLPP 300

Qy 121 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 190  
 Db 120 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 180

Qy 191 VELQETFGSALLSSRVLICESWPSDSYRAFTISLILVQYLPLVCLTVSHTSVRSISC 250  
 Db 190 QCVSVLVSTLILISIAIVRYMIKHPISNNLTANHGFLIATWTLGFAICSPLPVFHSL 190

Db 181 VELQETFGSALLSSRYLCLVESWPSD SYRAFTISLILLYOYLPLVCLTVSHTSYCRSIS C 240  
 Qy 251 GLSNKENRLEENEMINTLHSKXGSQPOVLSGSHKWS SFIKCHRRXSKKTCACVL PAP 310  
 Db 241 GLSNKENRLEENEMINTLHSKXGSQPOVLSGSHKWS SFIKCHRRXSKKTCACVL PAP 300  
 Qy 311 ERPSQENHSLRILPENFGSRSQSLSSSKF PGVPTCFEKPKEENSDVHBLRVRSVTRIK 370  
 Db 301 ERPSQENHSLRILPENFGSRSQSLSSSKF PGVPTCFEKPKEENSDVHBLRVRSVTRIK 360  
 Db 371 KRSRSVFYRLTILLYFAVSWMPLHLFHYTDFNDNLISNRHFKLVYCICHLJGMMSCL 430  
 Qy 361 KRSRSVFYRLTILLYFAVSWMPLHLFHYTDFNDNLISNRHFKLVYCICHLJGMMSCL 420  
 Db 361 KRSRSVFYRLTILLYFAVSWMPLHLFHYTDFNDNLISNRHFKLVYCICHLJGMMSCL 420  
 Db 431 NPILYGLNNGIQL 446  
 Db 421 NPILYGLNNGIQL 436  
 Search completed: June 7, 2005, 18:02:53  
 Job time : 151 secs

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RESULT 15  
 US-09-826-509-533  
 i Sequence 533, Application US/09826509  
 i Publication No. US20030204073A1  
 GENERAL INFORMATION:  
 i APPLICANT: Lehmann-Bruinsma, Karin  
 i APPLICANT: Lin, I-Lin  
 i TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G  
 i FILE REFERENCE: Protein-Coupled Receptors  
 CURRENT APPLICATION NUMBER: US/09/826,509  
 i CURRENT FILING DATE: 2001-04-05  
 i PRIOR APPLICATION NUMBER: 60/195,747  
 i PRIOR FILING DATE: 2000-04-07  
 i PRIOR APPLICATION NUMBER: 09/170,496  
 i PRIOR FILING DATE: 1998-10-13  
 i NUMBER OF SEQ ID NOS: 589  
 i SOFTWARE: Patentin Version 2.1  
 i SEQ ID NO: 533  
 i LENGTH: 445  
 i TYPE: PRT  
 i ORGANISM: Homo sapiens  
 US-09-826-509-533

Query Match 86.5%; Score 2262; DB 10; Length 445;  
 Best Local Similarity 99.3%; Pred. No. 2.4e-184;  
 Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11	MDLEDEYYNKTLATEENNTAAATRNSDFPVDDYKSSVDLQYFLIGLYTFVSLJGMGCNL 70
Db 1	MDLEDEYYNKTLATEENNTAAATRNSDFPVDDYKSSVDLQYFLIGLYTFVSLJGMGCNL 60
Qy 12	LILMALMKRNQKTTVNLIGNLAFSIDLVLFCSPTFTLISVLLDQMGKYMCHIMPL 130
Db 1	LILMALMKRNQKTTVNLIGNLAFSIDLVLFCSPTFTLISVLLDQMGKYMCHIMPL 120
Qy 13	QCVSYLVSTLILISTIAIVRYHMIRKPHISNLTANHGFYFLIATWTLGFAICSPLPVPHSL 190
Db 121	QCVSYLVSTLILISTIAIVRYHMIRKPHISNLTANHGFYFLIATWTLGFAICSPLPVPHSL 180
Qy 191	VELQETFGSALLSSRYLCVESWPSD SYRAFTISLILLYOYLPLVCLTVSHTSYCRSIS C 250
Db 181	VELQETFGSALLSSRYLCVESWPSD SYRAFTISLILLYOYLPLVCLTVSHTSYCRSIS C 240
Qy 251	GLSNKENRLEENEMINTLHSKXGSQPOVLSGSHKWS SFIKCHRRXSKKTCACVL PAP 310
Db 241	GLSNKENRLEENEMINTLHSKXGSQPOVLSGSHKWS SFIKCHRRXSKKTCACVL PAP 300
Qy 311	ERPSQENHSLRILPENFGSRSQSLSSSKF PGVPTCFEKPKEENSDVHBLRVRSVTRIK 370
Db 301	ERPSQENHSLRILPENFGSRSQSLSSSKF PGVPTCFEKPKEENSDVHBLRVRSVTRIK 360
Qy 371	KRSRSVFYRLTILLYFAVSWMPLHLFHYTDFNDNLISNRHFKLVYCICHLJGMMSCL 430

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	allatostatin recep neurokinin 2 recep glucocorticoid-ind eurokinin 1 recep hypothetical prote protein AC7.1 (imp neurokinin 1 recep hypothetical prote galanin receptor 1 neurokinin 1 recep neurokinin 3 recep probable allatosta neurokinin 1 recep neurokinin 3 recep hypothetical prote
Run on:	June 7, 2005, 17:49:36 ; Search time 41 Seconds (without alignments)	30 302.5 11.6 423 2 JC7677 31 300 11.5 424 1 S00516 32 300 11.5 443 2 D40470 33 299.5 11.4 407 2 S20304 34 298 11.4 519 2 S17783 35 297.5 11.4 365 2 T20184 36 295.5 11.3 390 2 B88684 37 295.5 11.3 407 1 JQ1274 38 295 11.3 539 2 T27559 39 294.5 11.3 349 2 I59336 40 293.5 11.2 407 2 A34357 41 293 11.2 465 1 JQ1517 42 292 11.2 357 2 JC7319 43 292 11.2 407 2 S23510 44 292 11.2 452 2 A34916 45 291 11.1 391 2 T32714
Title:	US-09-771-956-9	
Perfect score:	2616	
Sequence:	1 MSFYSKQDYNMFDLBDYNN.....KOASPVAFKINNNDDNEKI 499	
Scoring table:	BLOSUM62	
Searched:	GapOp 10.0 , Gapext 0.5	
Total number of hits satisfying chosen parameters:	283416	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100%	
Database :	PIR 79: 1: pir1: 2: pir2: 3: pir3: 4: pir4: SUMMARIES	
Result No.	Score	Query Match Length DB ID Description
1	771.5	29.5 384 2 A45490 neuropeptide Y/pep
2	740.5	28.3 382 2 B46133 neuropeptide Y/pep
3	739.5	28.3 382 2 S27388 neuropeptide Y rec
4	696.5	26.6 366 2 S71152 neuropeptide Y/pep
5	566	21.6 349 2 S12863 G protein-coupled
6	506	19.4 375 2 S63685 neuropeptide Y rec
7	506	19.3 375 2 I39182 pancreatic polypep
8	505	19.3 375 2 G02300 neuropeptide Y/pep
9	458	17.5 381 2 I39187 neuropeptide Y/pep
10	404	15.4 370 1 I52315 G protein-coupled
11	387	14.8 584 2 JC7809 sulfatokinin receptor
12	374	14.3 436 2 JC5599 cholecystokinin A
13	372	14.2 427 2 S50150 gastric CCK-A rece
14	365.5	14.0 444 2 A42685 cholecystokinin re
15	358.5	13.7 455 2 T15622 hypothetical prote
16	355	13.6 449 2 A41738 neuropeptide Y rec
17	353	13.5 447 2 A47430 Gastrin/cholecysto
18	353	13.5 428 2 JN0692 cholecystokinin ty
19	352.5	13.5 430 2 I51898 cholecystokinin A
20	345.5	13.2 453 2 S32817 Gastrin receptor -
21	341	13.0 452 2 JC2459 Gastrin/cholecysto
22	331	12.7 450 2 JQ1614 Gastrin receptor -
23	331	12.3 452 2 A46195 cholecystokinin B
24	322.5	12.3 398 1 J01059 neurokinin 2 recep
25	321.5	12.3 457 2 T29741 hypothetical prote
26	320	12.2 423 2 B40470 glucocorticoid-ind
27	315	12.0 399 2 T16277 hypothetical prote
28	310	11.9 384 2 A41007 gastrin-releasing
29	304.5	11.6 394 2 JC7209 Galanin receptor -

## ALIGNMENTS

Query Match	29.5%; Score 771.5; DB 2; Length 384;	Db	117 FVQCVSITVSISLVLIAVERHOLIINPRGWRDPNRHAYIGITIVIWLAVASSLPFVYQ 176
Best Local Similarity	34.7%; Pred. No. 4.7e-54;	Db	189 SIVELOQETFGSALLS--RYLCVEWSNPSDSYRIAFITSLLVQYIILPLVCLTVTSVHTSVC 245
Matches	170; Conservation	Db	177 IITD-EFFQNVSLAFAKDKYVCFDKPDSHRLSTTLLVQYFGLCFCIFICYFKI- 233
Qy	20 NKTL--ATENNNTA---ATRNSDFPVWDDYKSSVDLQYFLIGH-YTFVSLLGFMGNLLI 72	Db	246 RSISCGLSNKENLEENEMINLTLPSSKGSPQVKLSSSHKRSYFIIKKHRRYSKKTAC 305
Db	2 NSTLFSQVENDSVHNSNESEKNAQLAENDCHLPLAMMFTLALAYGAVITLGSGNL 61	Qy	234 ----- YIRIKKRNNNMMDK---- 246
Qy	73 LMLMKKRNQKTTVNEFLIGNLAFLSDILVVLFCSPPTLTSVLLDMEGKVMCHIMPELC 132	Db	234 ----- YIRIKKRNNNMMDK---- 246
Db	62 LLLIKQKENRKNVNTNLIVLNLSFSDLVLMCPLPTFVTLMDHWFGRAMCKLNPFYC 121	Qy	206 VLPAPERPSQENHSRILPENFGSVRSQLSSSSKFPIPGVPTCFEIKPEESENSDVHLYVRKS 365
Qy	133 VSVLVSTLILLISIAITVRYNIKHPISNNLTANHGFLIATWTWLGFALCSPLPVFHSLV 192	Db	247 ----- IRDSKYRSSE----- 256
Db	122 VSITYSISFLILIAVERHOLIINPRGWRDPNRHAYIGITIVIWL-AVASSLPFLIYQW 179	Qy	366 VTRIKKRRSRSVFYRITLILVFLAVASSLPFLHLPHVVTDFNDNLJSNRHFKLAYCICHLLGM 425
Qy	193 LQETFGSALLS--RYLCVEWSNPSDSYRIAFITSLLVQYIILPLVCLTVTSVCRSTS 249	Db	257 ----- TTKRINYMMLSITVAFACWLPPTINTVFDWNHQIATCNHNLFLUCLHTAM 309
Db	180 TDEPPQNVTIDAYKCYVCPDQFSPDSHRLSYTTLVQYFGLCFCIFICYFKI---- 234	Qy	426 MSCCLNPILYGFELNNNGIORDLOFFNFCDFRSRDDYETIANSTMHTDVSKTSLSKQASPV 485
Qy	250 CGLSKRNENLEENEMINLTLPSSKGSPQVKLSSSHKRSYFIIKKHRRYSKKTACVLA 309	Db	310 ISPCVNPFFYGFANKNFQRLQFFNFCDFRSRDDYETIANSTMHTDVSKTSLSKQASPV 369
Db	235 ----- YIRLKR 499	Qy	436 AFKKINNNDDNEK 499
Qy	310 PERPSQENHSRILPENFGSVRSQLSSSSKFPIGVPTCFEIKPEESENSDVHLYVRKS 369	Db	370 AFKKISMN-DNEK 382
Db	242 ----- NNMDKMRDNKYRSSE 257	RESULT 3	
Qy	370 KKRSSRSVFYRITLILVFLAVASSLPFLHLPHVVTDFNDNLJSNRHFKLAYCICHLLGMSC 429	Db	S27388 neuropeptide Y receptor NPY-1 - mouse
Db	258 TKR---INMILSIVVAFACWLPPTINTVFDWNHQIATCNHNLFLUCLHTAMISTIC 314	C:Species:	Mus musculus (house mouse)
Qy	430 INPILYGFELNNNGIORDLOFFNFCDFRSRDDYETIANSTMHTDVSKTSLSKQASPVARK 489	C:Accession:	S27388
Db	315 VNPIYGFLNKNFQRLQFFNFCDFRSRDDYETIANSTMHTDVSKTSLSKQASPVAFRK 374	R:Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.	
Qy	490 INNNDDENEK 499	DB:Leit.: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific exons	
Db	375 INNNDDENEK 384	A:Reference number: S27388; MUID:93106169; PMID:1468559	
A:Status: preliminary			
A:Molecule type: DNA			
C:Superfamily: neurokinin 1 receptor			
C:Cross references: UNIPROT:Q04573; EMBL:Z18280; NTID:953438; PIDN:CAA79157.1; PID:953439			
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Query Match 28.3%; Score 739.5; DB 2; Length 382;			
Best Local Similarity 33.4%; Pred. No. 1.7e-51;			
Matches 165; Conservative 76; Mismatches 126; Indels 127; Gaps 10;			
Db			
Qy 20 NKTL--ATENNNTA---ATRNSDFPVWDDYKDYQFLIGYTF----VSLIGFMG 68			
Db 2 NSTLFSKVENHSTHYNNSPLAFVN----DCDHLPPLAYFTALAYGAVILAVSYG 56			
Qy 69 NLILMALMKRNQKTTVNLFLIGNLAFLSDILVVLFCSPPTLTSVLLDQWMPGKVMCHIMP 128			
Db 57 NLALIIILKQEMRNTNLIVLNLSFSDLVAVMCLPFTFYTLMDHWGESETMCKLNP 116			
Qy 129 FLOCVSVLVLSTLILISIAITVRYHMKHPISNNLTANHGFYLATWTWLGAICSPLPVFH 188			
Db 117 FVQCVSITVSISLVLIAVERHOLIINPRGWRDPNRHAYIGITIVIWLAVASSLPFVYQ 176			
Qy 189 SIVELOQETFGSALLS--RYLCVEWSNPSDSYRIAFITSLLVQYIILPLVCLTVTSVHTSVC 245			
Db 177 IITD-EFFQNVSLAFAKDKYVCFDKPDSHRLSTTLLVQYFGLCFCIFICYFKI- 233			
Qy 246 RSISCGLSNKENLEENEMINLTLPSSKGSPQVKLSSSHKRSYFIIKKHRRYSKKTAC 305			
Db 234 ----- YIRIKKRNNNMMDK---- 246			
Qy 306 VLPAPERPSQENHSRILPENFGSVRSQLSSSSKFPIGVPTCFEIKPEESENSDVHLYVRKS 365			
Db 247 ----- IRDSKYRSSE----- 256			
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C:Sequence change: 1-382 <EVA>			
C:Accession: B46133			
C:Species: Mus musculus (house mouse)			
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000			
C:Accession: B46133			
C:Status: preliminary; not compared with conceptual translation			
C:Molecule type: nucleic acid			
C:Residues: 1-382 <HER3>			
C:Note: Sequence extracted from NCBI backbone (NCBIP:108539)			
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein			
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein			
Query Match 28.3%; Score 740.5; DB 2; Length 382;			
Best Local Similarity 33.6%; Pred. No. 1.4e-51;			
Matches 166; Conservative 74; Mismatches 127; Gaps 10;			
Db			
Qy 20 NKTL--ATENNNTA---ATRNSDFPVWDDYKSSVDLQYFLIGH-YTFVSLLGFMGNLLI 72			
Db 2 NSTLFSRVENHSTHYNNSPLAFVN----DCDHLPPLAYFTALAYGAVILAVSYG 56			
Qy 69 NLILMALMKRNQKTTVNLFLIGNLAFLSDILVVLFCSPPTLTSVLLDQWMPGKVMCHIMP 128			
Db 57 NLALIIILKQEMRNTNLIVLNLSFSDLVAVMCLPFTFYTLMDHWGESETMCKLNP 116			
Qy 129 FLOCVSVLVLSTLILISIAITVRYHMKHPISNNLTANHGFYLATWTWLGAICSPLPVFH 188			

Db	257	-----TKRINIMLISIVVAFAYCWLPLITNTFEDWNFIQIATCNHNLFLCHLTAM	309	Db	315	YGFLNKRNFORDLQFFFNFCDRSREDDYETIAMSTMHTDVSKTSLQASPIA	366
Qy	426	MSCCLNPLYGLANGIQLQQFFNFCDFRSRDDYETIAMSTMHTDVSKTSLQASPV	485	RESULT 5			
Db	310	ISTCVNPYIIFYGFLNKNFQRDQQFFNFCDFRSRDDYETIAMSTMHTDVSKTSLQASPV	369				
Qy	486	AFKKINNNNDNEKEI	499	C;Species: Rattus norvegicus (Norway rat)			
Db	370	AFKKISMN-DNEKV	382	C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004			
Qy				C;Accession: S12863; S19101			
Db				R;Eva, C.; Keinonen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.			
				FEBS Lett. 271, 81-94, 1990			
				A;Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the G protein-coupled receptor family			
				A;Reference number: S12863; PMID:91032093; PMID:2172008			
RESULT 4				A;Accession: S12863			
	S71152	neuropeptide Y/peptide YY receptor Y1 - African clawed frog		A;Molecule type: mRNA			
		Cross-references: Xenopus laevis (African clawed frog)		A;Residues: 1-49 <PVA>			
		A;Experimental source: brain, hypothalamus		A;Cross-references: UNIPROT:P34992; ENBL:L25416; NID:9409169; PID:AAA49918.1; PMID:94091			
		R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.		C;Superfamily: neurokinin 1 receptor			
		Biochim. Biophys. Acta 1261, 439-441, 1995		C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane			
		A;Title: Cloning and sequencing analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA		F:39-61/Domain: transmembrane #status predicted <TM1>			
		A;Reference number: S55924; PMID:742373		F:73-93/Domain: transmembrane #status predicted <TM2>			
		A;Accession: S55924		F:114-125/Domain: transmembrane #status predicted <TM3>			
		A;Status: preliminary; nucleic acid sequence not shown		F:155-175/Domain: transmembrane #status predicted <TM4>			
		A;Molecule type: mRNA		F:211-231/Domain: transmembrane #status predicted <TM5>			
		A;Residues: 1-278 'T' 280-366 <BL0>		F:262-285/Domain: transmembrane #status predicted <TM6>			
		A;Cross-references: ENBL:L25416; NID:9409169		F:299-322/Domain: transmembrane #status predicted <TM7>			
		C;Superfamily: neurokinin 1 receptor		F:2,11,17/Binding site: carbohydrate (Asn) (covalent) #status predicted			
		C;Keywords: G protein-coupled receptor; transmembrane protein		F:34/Binding site: phosphate (Thr) (covalent) #status predicted			
		Query Match 26.6% Score 696.5; DB 2; Length 366; Best Local Similarity 32.6%; Pred. No. 4.4e-48; Matches 154; Conservative 76; Mismatches 127; Indels 115; Gaps 8;		Query Match 21.6% Score 566; DB 2; Length 349; Best Local Similarity 28.4%; Pred. No. 1.1e-37; Matches 129; Conservative 73; Mismatches 126; Indels 126; Gaps 9;			
Qy	19	YNKTLATEENNTAAATRNNSDFFPWDDYKSSVDLQYFLIGLI-YTFVSLLGFMGNLJILMAM	77	Qy 20 NKTL-ATENNTAATRNNSDFFPWDDYKSSVDLQYFLIGLI-YTFVSLLGFMGNLJILMAM	68		
Db	6	YFNFLSPVNISG--NITPUSIDEDCALPLP--MIFTLLALAYGAVTLGLSGNLALIIII	61	Db 2 NSTLFLSERVENSVHVNSENPSFLAEN----DDCHLPLAVFTLALAYGAVTLGLSGNLALIIII	56		
Qy	78	KRNQKTTVNWFLIGNLATESDILVFLFCSPPTLTSVLLDQMGFMCHIMPFLQCVSIVL	137	Qy 69 NLLILMALMCKERNQKTTVNWFLIGNLATESDILVFLFCSPPTLTSVLLDQMGFMCHIMPFLQCVSIVL	128		
Db	62	KQEMRNNTVNLIVNLNSFSDLLATIMCPLPTLYLTDWMIIGEVMKLNBYIQCVSIVL	121	Db 57 NLALIILLQKEMRNNTVNLNSFSDLLATIMCPLPTLYLTDWMIIGEVMKLNBYIQCVSIVL	116		
Qy	138	STLILSIAIVRYHMKHPISNNNLTAHNGYFLIATWVTLGFAICSPPLPVHSLYLQETPF	197	Qy 129 FLQCYSVLVLSTLILSIAIVRYHMKHPISNNNLTAHNGYFLIATWVTLGFAICSPPLPVHSLYLQETPF	188		
Db	122	SITSLVLIAERHLIINPRGWNRNHRACFGTVIWGPMACSTPLMNYSVLTD-BEPF	179	Db 117 FVQCVSITVSIFSLVLAVERHOLINPSLQVWVGETMCKLNP	116		
Qy	198	GSALLSS---RYLCVSEWSPDSYRIAPTISLLVQYLPLVCLTVSHTSVCRS1SCGSLN	254	Qy 189 SLVLFDTFGALLSS---RYLCVSEWSPDSYRIAPTISLLVQYLPLVCLTVSHTSVCRS1SCGSLN	245		
Db	180	KNTSLDSYIGKVYCYCLEDFPDKFRSLSYTLLFLQYLGPKCFIVPCYCTKLI	229	Db 177 ILTD--EPFQNSVSLAFKDQYVCDFKPSDSHRLSYTLLVQYLGPKCFIVPCYCTKLI	233		
Qy	255	KENRLEENMINLTLHPSKRGPOVKLSGSRKHWSYSFIRKHRRYSSKTCVLPAPERS	314	Qy 246 RSISCGLSNKENRLEENMINLTLHPSKKGSPQVKLSGSHKWSYSPTKGHRRYSSKTCVLPAPERS	305		
Db	230	-----PLRKRR-----PLRKRR-----PLRKRR-----PLRKRR-----PLRKRR-----	236	Db 234 -----YIRKRRNNMMDDK-----YIRKRRNNMMDDK-----YIRKRRNNMMDDK-----	246		
Qy	315	QENHSRILPENFGSVRSQSLSSSKF1PQVTCBEIKPERNSDVHELRVKRKS1TRIKRKS1	374	Qy 306 VLPAPERPSQENHSR1LPENFGSVRSQSLSSSKF1PQVTCBEIKPERNSDVHELRVKRKS1	365		
Db	237	-----NMMMDKIRDNYRSSETRK-----NMMMDKIRDNYRSSETRK-----NMMMDKIRDNYRSSETRK-----	255	Qy 366 VTRIKRKS1F1YR1LILYFAVSMPLHFLHVTDNDNL1SNRHFKLVYCICHLMGMSCLNPIL	425		
Qy	375	SVFYRFLTLLVFAVSMPLHFLHVTDNDNL1SNRHFKLVYCICHLMGMSCLNPIL	434	Db 257 -----TRKINMLISIVVAVCWLPLTNTVFDWNHQIATCNHNLFLCLHTAM	309		
Db	256	-INTMLLSIVVGFLCWLPF1NUFWDNHEAVTCNLFLCHLTAMISTCVCNP1F	314	Qy 426 MSCCLNPLYGLANGIQLQQFFNFCDFRSRSDYETIAMSTMHTDVSKTSLQASPIA	459		
Qy	435	YGFLNKRNFORDLQFFFNFCDRSREDDYETIAMSTMHTDVSKTSLQASPIA	486	Db 310 ISTCVP1F1YR1LILYFAVSMPLHFLHVTDNDNL1SNRHFKLVYCICHLMGMSCLNPIL	343		

RESULT 6		Query Match Score 19.3%; Best Local Similarity 25.2%; Matches 112; Conservative 25.2%; Pred. no. 7, 9e-33; Mismatches 123; Indels 114; Gaps 7;
S6385	neuropeptide Y receptor D type - mouse	
C;Species: Mus musculus (house mouse)		
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004		
C;Accession: S63685		
R;Gregor, P.; Millham, M.L.; Feng, Y.; Decarr, L.B.; McCaleb, M.L.; Cornfield, L.J.		
PES Lett. 381, 58-62, 1996		
A;Title: Cloning and characterization of a novel receptor to pancreatic polypeptide, a		
A;Reference number: S63685; MUID:36193913; PMID:8641140		
A;Accession: S63685		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-375 <GRE>		
A;Cross-references: UNIPROT:061041; EMBL:U40189; PIDN:AA5C2442.1; PID:9122		
C;Superfamily: neurokinin 1 receptor		
Query Match Score 19.4%; Best Local Similarity 25.6%; Matches 115; Conservative 25.6%; Pred. no. 7, 2e-33; Mismatches 137; Indels 125; Gaps 6;		
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Db 39 ELLAPLITVSIETLGVNLCLIFVTTRQEKSISNTVNLIANLAFLSPMLCICQPLT 98	Db 39 ELLAPLITVSIETLGVNLCLIFVTTRQEKSISNTVNLIANLAFLSPMLCICQPLT 98	
Qy 109 LTSVLDQNMFGKVMCHIMPFLQCVSFLVSTLILLISIAIVRYHMIKHPISNNLTANHGF 168	Qy 109 LTSVLDQNMFGKVMCHIMPFLQCVSFLVSTLILLISIAIVRYHMIKHPISNNLTANHGF 168	
Db 99 VTYTIMDYNFLGEVLCRMNFIQCMSTVTSILSVLVALERHOLIINPQGWKEISIQAYL 158	Db 99 VTYTIMDYNFLGEVLCRMNFIQCMSTVTSILSVLVALERHOLIINPQGWKEISIQAYL 158	
Qy 169 LIATWTLGFAICSPSL--PVFH---SLVLEQTFGSALLSSRXYLVCWSWPSDSY 217	Qy 169 LIATWTLGFAICSPSL--PVFH---SLVLEQTFGSALLSSRXYLVCWSWPSDSY 217	
Db 159 GIVVWEIFSCSFLPLANTSLNDLFLHNSKVKY--FLEDKVCFYFWSSPH 210	Db 159 GIVVWEIFSCSFLPLANTSLNDLFLHNSKVKY--FLEDKVCFYFWSSPH 210	
Qy 218 RIAFTISLILVQYTFPLVCHLTVTSVTSISCGLSNKERNLEENMINLTLPSSKGSP 277	Qy 218 RIAFTISLILVQYTFPLVCHLTVTSVTSISCGLSNKERNLEENMINLTLPSSKGSP 277	
Db 211 PLIYTFLFLFOYCPLAFLVCFYTRIYRL--241	Db 211 PLIYTFLFLFOYCPLAFLVCFYTRIYRL--241	
RESULT 8		
Qy 278 QVKLGSKHKWYSYSPFKHHBRRYSKTKTACVLPAAPERPSQENHSRILPENFGSVRSQQLSSS 337	Qy 278 QVKLGSKHKWYSYSPFKHHBRRYSKTKTACVLPAAPERPSQENHSRILPENFGSVRSQQLSSS 337	
Db 242 -----ORQHVFHAHCSSRAGQM-----260	Db 242 -----ORQHVFHAHCSSRAGQM-----260	
- Qy 338 KFPGVPTCPCEIKPBENSVDHELRVKSRTRIKERSRSYFYRTRLILVPAVSMMPHLF 397	- Qy 338 KFPGVPTCPCEIKPBENSVDHELRVKSRTRIKERSRSYFYRTRLILVPAVSMMPHLF 397	
Db 261 -----KRINM--IATMVTAAFAVWLPFLPF 284	Db 261 -----KRINM--IATMVTAAFAVWLPFLPF 284	
Qy 398 RHTTDENDLJSNRHFKLGYCICHILGMNSCCLNPFLYGLNGIQRDQFFPNFCDFRS 457	Qy 398 RHTTDENDLJSNRHFKLGYCICHILGMNSCCLNPFLYGLNGIQRDQFFPNFCDFRS 457	
Db 285 NTLEDWYQEAIPACHGNLFLMCHLAMASTCVPFIYGLNINFKDIAKVLITCHCRS 344	Db 285 NTLEDWYQEAIPACHGNLFLMCHLAMASTCVPFIYGLNINFKDIAKVLITCHCRS 344	
Qy 458 RDDDYETIAMSTMTHDVSTKSLRQASPVAF 487	Qy 458 RDDDYETIAMSTMTHDVSTKSLRQASPVAF 487	
Db 345 PGGBSEHPLUSTVHTDLSGSMRNGSKSNP 374	Db 345 PGGBSEHPLUSTVHTDLSGSMRNGSKSNP 374	
RESULT 7		
I39182	neuropeptide Y/peptide YY receptor Y4 - human	
C;Species: Homo sapiens (man)		
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004		
C;Accession: I39182		
R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.		
J. Biol. Chem. 270, 26762-26765, 1995		
A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic		
A;Reference number: I39182; MUID:96070761; PMID:7592911		
A;Accession: I39182		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-375 <RES>		
A;Cross-references: UNIPROT:P50391; EMBL:U42387; PIDN:AA5C0280.1; PID:91063629		
C;Superfamily: neurokinin 1 receptor		
C;Keywords: appetite		



Db	270 R-----ARRRTFCL 279	QY	442 IQR 444
Qy	380 LTILLVPAISWMPHLFLHFTDNDNLISNRHFKLVICLCHLGMSSCLNPLIGFLN 439	Db	494 FRR 496
Db	280 LvvvvvveALCWLPFLHFLNRLDPRALDPYAFGLVQLLCHWLAMSSACYNPTIYAWH 339		
Qy	440 NGIQBDLQ 447		
Db	340 DSFREBLR 347		
<b>RESULT 12</b>			
	JCS599 cholcytokinin- $\Lambda$ receptor - mouse		
C;Species:	Mus musculus (house mouse)		
C;Date:	23-Sep-1997 #sequence_revision 21;-Sep-1997 #text_change 09-Jul-2004		
C;Accession:	JCS599		
C;Species:	Drosophila melanogaster		
C;Date:	03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004		
C;Accession:	JC7809		
R;Kubiak, T.M.; Larsen, M.J.; Burton, K.J.; Banow, C.A.; Martin, R.A.; Zantello, M.R.; Title: Cloning and functional expression of the first Drosophila melanogaster sulfakinin receptor protein, DSK-R1 - fruit fly (Drosophila melanogaster) A;Title: Cloning and functional expression of the first Drosophila melanogaster sulfakinin receptor protein, DSK-R1 - fruit fly (Drosophila melanogaster) A;Accession: JC7809 A;Cross-references: UNIPROT:Q7M3J6; GB:AX128640 A;Residues: 1-584 <KUB> A;Comments: This receptor, the first functionally active orphan Drosophila sulfakinin G-protein coupled receptor, is a member of the seven transmembrane G-protein coupled receptor family. It shows a high degree of sequence identity with the Drosophila melanogaster sulfakinin receptor (residues 1-467). It is predicted to contain a single transmembrane domain and a large extracellular N-terminal domain. A;Genetics: A;Gene: dsk-r1 A;Map position: 17 F;115-139/Domain: transmembrane region #status predicted <TMR1> F;149-167/Domain: transmembrane region #status predicted <TMR2> F;189-207/Domain: transmembrane region #status predicted <TMR3> F;229-255/Domain: transmembrane region #status predicted <TMR4> F;275-300/Domain: transmembrane region #status predicted <TMR5> F;411-454/Domain: transmembrane region #status predicted <TMR6> F;467-491/Domain: transmembrane region #status predicted <TMR7>			
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A;Map position: 17			
F;115-139/Domain: transmembrane region #status predicted <TMR1>			
F;149-167/Domain: transmembrane region #status predicted <TMR2>			
F;189-207/Domain: transmembrane region #status predicted <TMR3>			
F;229-255/Domain: transmembrane region #status predicted <TMR4>			
F;275-300/Domain: transmembrane region #status predicted <TMR5>			
F;411-454/Domain: transmembrane region #status predicted <TMR6>			
F;467-491/Domain: transmembrane region #status predicted <TMR7>			
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Best Local Similarity	25.1%	Pred. No. 3.e-22;	
Matches	110;	Conservative	82; Mismatches 177; Indels 70; Gaps 13;
Qy	23 LATENNATAATRNSDFPYWDYKSYSDVILQYFLIGPSVSLIGFMGNPILILMALKRNQ	Db	20 LGHENETIFCLDOPQPS KEWQSAQV 1-----LYSIFPLISVLGNTLVITLRNKR 72
Qy	83 KTTVNFLIGNLNAPSDLIVLFLFCSPFTHTSVLLDQWMFGKVMCHIMPEFLQCVSYVLSTLIL 142	Db	73 RTVTNIFELSLAVSDMLCLFCMPNFI.IPNLXKDFFIRGSAVCKTTYEMGTTSVSVTFNL 132
Qy	143 ISTAVRYXMHKPISNL-TANHGFELIATWTHGFAISPLPVPHSLVLEQTFGSA 200	Db	133 VASLERYGAICRPLQSNWQTKSHAIKVIAATWCSETIMTPYPIVSNLVPTKNNNOT 192
Qy	201 LISSRYLCVESWPSDSYRAFTSLLIVQYIPLVLCTVTSVRSITSGSLSNKENRNL 260	Db	193 ANMCFELL----PSDAMQOSWQTFLILFLFIPGVNVAYGUISLEYQIKFDASQ-- 246
Qy	261 ENMINLTLPHKSKGSGPQYKLS--GHKWSYSPIKHRRYSKKTACVLPAPERPSQEN 317	Db	247 -----KXSAKEKRLSSGGCGGGSSS----SRYEDSDGCYLQKSRRPKLE 288
Qy	318 HSRLIPENFGSVPRSQSSSSKTPVQHVTCKFEIKPBNSDVHHLRVKSVTRIKKRSRSVF 377	Db	289 -----LQQLTSS-----SGGRINRIRSSSAANLIAKRR-VI 320
Qy	378 YRUTLILYFAYSWMPMPLHFLHVVTDFP.DNLISRHFK--LYVCICHLGMMSCCLNPL 434	Db	321 RMILIVVUFLCWMPMIFSANAWRAY. DTVSAEKHLSGTCPISFIL--LISVTRSSCVNPIL 377
Qy	435 YGFLNGIQRDLOFFENPC 453	Db	378 YCPFMKRPRLGFMATPPCC 396
<b>RESULT 13</b>			
Db	550150		
Qy	345 TCFBI-----KPEENSDVHFLYKRS---VTRIKKRSRSVYFLRFLILLYFAVS 390		
Db	386 TVIITTTTIVTLAKTSSSIVRDAALRSNEARTLKKR--VVWMLFLVLEFFIC 442		
Qy	391 WMPFLHFLF-----WTFDEND-NLISNRHFKLVICLCHLGMSSCLNPLIGFLNNG 441		
Db	443 WTPLYINTVMVLIGPVVVEYDVTAS-----FLQLAYSSCNPITYCFMNA 493		
A;Title:	Cloning and expression of the rabbit gastric CCK-A receptor.		



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Query Match      13.7%; Score 358.5; DB 2; Length 455;
Best Local Similarity 22.5%; Pred. No. 6.4e-21;
Matches 105; Conservative 73; Mismatches 160; Indels 129; Gaps 12;
Matches 105; Conserv. 73; Mismatches 160; Indels 129; Gaps 12;

Qy   46 SVDDLQFLIGLYTFSVLGPMGNLLILMALMQRNQKTVNLIGLNLFASDILVLFPS 105
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    34 SPKEFGYFIFPAAYMLILEGAINFTIVIVLNPAMRTRNFPFLNLALSDFVCTVA 93
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy   106 PFTLTSVLDLDMFGRKVMCHIMPFLQCVSVLVSLTLLISTIAIVRYHMIKHPISNNLTANH 165
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    94 PTTLTLYLVNWPFSRTLICKTAGS!QGPNFLSISIAMSADRVYLIFPTTRERQQL 153
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy   166 GYFLIATWTLGFAICSPL-----PVTFLSVELQETFGSALLSSRYCVES --WPSD 215
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   154 SFCFFIMIWTLISLILAVPLIQASDLITPVF ----VBPSCLAL ---YCHEQNBIWEM 204
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy   216 SY-RIAFITISLILVQXILPLVCLTVSHTSYCRSISCGLSNKENLEENMINLTLPSSK 274
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   205 IISKGTYTLAVLITYQAFPLSLVDAYSRTAHRMKLRFANR----NQVNTNTNTSQR 258
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy   275 SGPOVKLSGSHKWSYSFIKGHRRYSKKTACVLPIAPERQSQENHSRILBENFGSQLS 334
Db   259 ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- 258
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy   335 SSSKFTIPGVPTCFIEKPEENSDVHRLVRSVTRIKRSRSVFYRLTILLVPAVSMPY 394
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   259 ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- 287
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
     RSVV --ERRORTHLVCAVAVAWIPL 287

Qy   395 HLFHVVTDFNDNLISNRHFKLVYCYCHLGMMSCLNPILYGLINNGLORDLQFFENFC 454
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   288 NVFH1---FNTFELVNSFSVTTFSICHCLAMCSAGLNPLIYAFFNNPFLIEFMHLDVG 344
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy   455 FRSRD---DDYETTAMSTPHTDVSK---TSLKQASPAPFKLNN 493
     | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   345 LRSLRVVIPEGESLKK-MRTEFRSGCCKTVTTAEPAUTORMNES 390
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Search completed: June 7, 2005, 17:59:31  
 Job time : 44 secs

Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Searched: 1612378 seqs, 512079187 residues							
Total number of hits satisfying chosen parameters:							1612378
Minimum DB seq length: 0							Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%							Maximum Match 100%
Listing first 45 summaries							
Database :	UniProt_03:*						
	1: uniprot_sprot:*						
	2: uniprot_trembl:*						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description		
1	2326	88.9	455	1 NY5R_HUMAN	Q15761 homo sapien		
2	2262	86.5	445	2 Q9GK73	Q9gk73 macaca mulu		
3	2188	83.6	446	2 Q925F1	Q925f1 cavia porce		
4	2177	83.2	446	1 NY5R_CANFA	062729 canis famili		
5	2016.5	77.8	456	1 NY5R_RAT	063634 rattus norvegicus		
6	2022	77.3	466	1 NY5R_MOUSE	070342 mus musculus		
7	1976	75.5	446	1 NY5R_PIG	097969 sus scrofa		
8	1603.5	61.3	443	2 Q8QFM2	08qfm2 gallus gallus		
9	771.5	29.5	384	1 NY1R_HUMAN	P25929 homo sapien		
10	761	29.1	382	1 NY1R_CANFA	Q02813 canis famili		
11	752	28.7	383	2 Q9GK75	Q9gk75 macaca mulu		
12	740.5	28.3	382	1 NY1R_RAT	P21555 rattus norvegicus		
13	740	28.3	383	1 NY1R_PIG	Q02835 sus scrofa		
14	739.5	28.3	382	1 NY1R_MOUSE	Q04573 mus musculus		
15	724.5	27.7	383	1 NY1R_CAVPO	Q9wvdo cavia porce		
16	707.5	27.0	385	2 OBOFMI	Q8qfm1 gallus gallus		
17	696.5	26.6	366	1 NY1R_XENLA	P34992 xenopus laevis		
18	617.5	23.6	377	2 O73733	Q73733 brachydanio		
19	582.5	22.3	348	2 Q6Y6A4	Q6y6a4 squalus acanthias		
20	558	21.3	348	2 Q6Y6A5	Q6y6a5 squalus acanthias		
21	546	20.9	371	1 NY6R_MOUSE	Q61212 mus musculus		
22	545.5	20.9	371	1 NY6R_RABBIT	P79217 orcto lagus		
23	536.5	20.5	377	2 Q8QGM3	Q8qgm3 gallus gallus		
24	512.5	19.6	371	2 Q6T6A6	Q6y6a6 squalus acanthias		
25	512	19.6	365	2 Q8UVW7	Q8uvw7 lampetra fluviatilis		
26	511	19.5	375	1 NY4R_RAT	Q63347 rattus norvegicus		
27	506.5	19.4	375	1 NY4R_MOUSE	Q61041 mus musculus		
28	506	19.3	375	1 NY4R_HUMAN	P50391 homo sapiens		
29	506	19.3	375	2 Q6FH06	Q6fh06 homo sapiens		
30	504.5	19.3	375	2 Q8YHV0	Q6yhv0 macaca mulatta		
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AC	Q15761; Q92916;						
DT	01-NOV-1997 (Rel. 35, Created)						
DT	01-NOV-1997 (Rel. 35, Last sequence update)						
DT	25-OCT-2004 (Rel. 45, Last annotation update)						
DB	Neuropeptide Y receptor type 5 (NPY5-R) (NPY5-Y receptor)	(Y5)					
DE	receptor (NPY5).						
RA	Gerald C., Walker M.W., Cribstone L., Gustafson E.L., Batzli-Harmann C., Smith K.E., Vayse P., Durkin M.M., Laz T.M., Linemeyer D.L., Schaffhausen A.O., Whitebread S., Hoffbauer K.G., Taber R.I., Branche T.A., Weinshank R.L.; Hoffbauer K.G.,						
RA	"A receptor subtype involved in neuropeptide Y-induced food intake."						
RA	Nature 382:168-171(1996).						
RA	SEQUENCE FROM N.A.						
RC	SEQUENCE OF 11-455 FROM N.A.						
RA	MEDLINE=96317559; PubMed=8700207; DOI=10.1018/jbc.2002.142.26040;						
RA	GERALD C., WALKER M.W., CRIBSTONE L., GUSTAFSON E.L., BATZLI-HARMANN C., SMITH K.E., VAYSE P., DURKIN M.M., LAZ T.M., LINEMEYER D.L., SCHAFFHAUSEN A.O., WHITEBREAD S., HOFFBAUER K.G., TABER R.I., BRANCHE T.A., WEINSHANK R.L.; HOFFBAUER K.G., NATURE 382:168-171(1996).						
RA	SEQUENCE OF 11-455 FROM N.A.						
RA	MEDLINE=964216516; PubMed=8824284; DOI=10.1074/jbc.271.42.26044;						
RA	HU Y., BLOMQVIST B.T., CORNFIELD L.B., DECARR L.B., FLORES-RIVEROS J.R., FREDLMAN L., JIANG P., LEWIS-HIGGINS L., SADOWSKI Y., SCHAEFER J., VELAZQUEZ N., MCCALEB M.L.; "Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior.", J. Biol. Chem. 271:26315-26319(1996).						
RA	SEQUENCE OF 11-455 FROM N.A.						
RA	MEDLINE=97312586; PubMed=9169127; DOI=10.1006/geno.1997.4684;						
RA	HERZOG H., DARBY K., BALL H., HORT Y., BECK-SICKINGER A., SHINE J., "Overlapping gene structure of the human neuropeptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation.", Genomics 41:315-319(1997).						
RA	SEQUENCE OF 11-455 FROM N.A.						
RA	CDSNA CLONES OF HUMAN PROTEINS INVOLVED IN SIGNAL TRANSDUCTION SUBMITTED BY THE GUTHRIE CDNA RESOURCE CENTER (WWW.CDNA.ORG).";						
RA	JUN-2003 TO THE EMBL/GENBANK/DBJ DATABASES -1- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyl cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders.						
RA	KOPATZ S.A., KRONSTEIN R.S., SHARMA S.V., "CDNA CLONES OF HUMAN PROTEINS INVOLVED IN SIGNAL TRANSDUCTION SUBMITTED BY THE GUTHRIE CDNA RESOURCE CENTER (WWW.CDNA.ORG).";						
RA	JUN-2003 TO THE EMBL/GENBANK/DBJ DATABASES -1- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyl cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders.						
RA	-1- SUBCELLULAR LOCATION: Integral membrane protein.						
RA	-1- TISSUE SPECIFICITY: Brain; hypothalamus						
RA	-1- SIMILARITY: Belongs to the G-Protein coupled receptor 1 family.						

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DR EMBL; AAC50623.1; .  
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DR MIM; 602001; .  
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DR GO; GO:0004983; F:neuropeptide Y receptor activity; TAS.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.  
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DR InterPro; IPR000393; NPYS receptor.  
DR InterPro; IPR000611; NPYS receptor.  
DR Pfam; PF00001; 7tm\_1\_1.  
DR PRINTS; PR00237; GPCR\_RHODOPSN.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; FALSE\_NEG.  
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KW Phosphorylation; Transmembrane.  
DOMAIN 1 50 Extracellular (Potential).  
FT TRANSMEM 51 72 1 (Potential).  
FT TRANSMEM 73 84 Cytoplasmic (Potential).  
FT TRANSMEM 85 105 2 (Potential).  
FT DOMAIN 106 125 Extracellular (Potential).  
FT TRANSMEM 126 147 3 (Potential).  
FT DOMAIN 148 167 Cytoplasmic (Potential).  
FT TRANSMEM 168 188 4 (Potential).  
FT DOMAIN 189 220 Extracellular (Potential).  
FT TRANSMEM 221 242 5 (Potential).  
FT DOMAIN 243 378 Cytoplasmic (Potential).  
FT TRANSMEM 379 401 6 (Potential).  
FT DOMAIN 402 414 Extracellular (Potential).  
FT TRANSMEM 415 438 7 (Potential).  
FT DOMAIN 439 455 Cytoplasmic (Potential).  
FT CARBOHYD 20 20 N-linked (GlcNAc . . ) (Potential).  
FT CARBOHYD 27 27 N-linked (GlcNAc . . ) (Potential).  
FT DISULFID 124 208 By similarity.  
FT LIPID 452 452 S-palmitoyl cysteine (Potential).  
SEQUENCE 455 AA; 51990 MW; 956274 BE5FB8FF CRC64;

Query Match 88.9%; Score 2326; DB 1; Length 455;  
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Matches 444; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFYSKQDYMMDLEDEYYNKTLATEENNTAAATRSDPEWDDYKSSYDDQYFLIGHYTF 60  
Db 1 MSFYSKQDYMMDLEDEYYNKTLATEENNTAAATRNSDFPWDDYKSSYDDQYFLIGHYTF 60  
Qy 61 VSLIGPMGNLILMALMKRNQKTVNLIGNLAFLDIIVLRCSPFTITSVLDQWNG 120  
Db 61 VSLIGPMGNLILMALMKRNQKTVNLIGNLAFLDIIVLRCSPFTITSVLDQWNG 120  
Qy 121 KVMCHIMPFLOCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGFLIATWTLGFAI 180  
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Qy 181 CSPLFVFHSIVELQFTGSAASSRLCYTESWPSDSYRAFTSSLILQYLPLVCLTVS 240  
Db 181 CSPLFVFHSIVELQFTGSAASSRLCYTESWPSDSYRAFTSSLILQYLPLVCLTVS 240  
Qy 241 HTSVCRSISGGLSNKENRLENEMINLTHPSKSGPQKLSSHKWSYSPFKHARRY 300  
Db 241 HTSVCRSISGGLSNKENRLENEMINLTHPSKSGPQKLSSHKWSYSPFKHARRY 300  
Qy 301 KRTACVLPAPERPSOBHNRLPENFGSRSQSLSSSKTPGVPCTCFBKPEENSDVHL 360

Db 301 KRTACVLPAPERPSOBHNRLPENFGSRSQSLSSSKTPGVPCTCFBKPEENSDVHL 360  
Qy 361 RVKESVTIKRKRSDFVFRLLILVAVSWMPMLHFLFVVTDNDNLISNRHFKLVYCIC 420  
Db 361 RVKESVTIKRKRSDFVFRLLILVAVSWMPMLHFLFVVTDNDNLISNRHFKLVYCIC 420  
Qy 421 HLLGMSCCLNPLIFYGLNNGIORDL 446  
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RESULT 2  
Q9GR73 ID Q9GR73 PRELIMINARY; PRT; 445 AA.  
AC Q9GR73; DT 01-MAR-2001 (TREMBLrel. 16, Created,  
AC Q9GR73; DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
AC Q9GR73; DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Neuropeptide Y receptor Y5.  
OS Macaca mulatta (Rhesus macaque).  
OC Bivalvia; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=954;  
RN [1]

RP SEQUENCE FROM N\_A. PMID:21184974; PubMed:11287098; DOI=10.1016/S0196-9781(01)00336-9;  
RX GO; GO:0001601; C:Integral to membrane; IBA.  
RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,  
RA Gackenheimer S., Johnson D., Beaver L.S., Gadski R.A., Baez M.;  
RT "Cloning and characterization of Rhesus monkey neuropeptide Y receptor subtypes(1)." ;  
RT Peptides 22:343-350 (2001).  
RL EMBL; AF303091; AAG0473.1; .  
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IBA.  
DR GO; GO:0004872; F:receptor activity; IBA.  
DR GO; GO:0001594; F:rhodopsin-like receptor activity; IBA.  
DR GO; GO:0007218; F:neuropeptide signaling pathway; IBA.  
DR InterPro; IPR000276; GPCR\_Rhodopsin.  
DR InterPro; IPR000393; NPYS\_receptor.  
DR InterPro; IPR000611; NPYS\_receptor.  
DR Pfam; PF000001; 7cm 1. 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSN.  
DR PRINTS; PR01016; NPFPETIDEXYR.  
DR PRINTS; PR01012; NPFPETIDEXYR.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Neuropeptide; Receptor.  
SEQUENCE 445 AA; 50812 MW; AEADACD259675BC93 CRC64;  
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Qy 71 LIIMLAIIKKKRQKTTVNLIGNLAFLDIIVLRCSPFTITSVLDQWNGMCHIMPFL 130  
Db 61 LIIMLAIIKKKRQKTTVNLIGNLAFLDIIVLRCSPFTITSVLDQWNGMCHIMPFL 120  
Qy 131 QCYSVLSVTLILISIAIVRYHMIKHPISNNLTANHGFLIATWTLGFAI CSPLPFHSL 190  
Db 121 QCYSVLSVTLILISIAIVRYHMFLIATWTLGFAI CSPLPFHSL 180  
Qy 191 VELQETFGSALLSSRLCYTESWPSDSYRAFTSSLILQYLPLVCLTVSITSVRSISC 250  
Db 181 VELQETFGSALLSSRLCYTESWPSDSYRAFTSSLILQYLPLVCLTVSITSVRSISC 240  
Qy 251 GLSNKENRLENEMINLTHPSKSGPQKLSSHKWSYSPFKHARRY 310  
Db 241 GLSNKENRLENEMINLTHPSKSGPQKLSSHKWSYSPFKHARRY 300

Qy	311 ERPSQENTHSRILPENFGSVRSQLSSSSKKFIPGVPCTPEIKPEENSVDYELRKRSVTRIK	370	Qy	KRSRSVFYRLTILYLIVFAVSMPPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMSCCL	430	
Db	301 ERPSQENHRSLPENFGSVRSQLSSSSKKFIPGVPCTPEIKPEENSVDYELRKRSVTRIK	360	Db	KRSRSVFYRLTILYLIVFAVSMPPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMSCCL	420	
Qy	371 KRSRSVFYRLTILYLIVFAVSMPPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMSCCL	430	Qy	KRSRSVFYRLTILYLIVFAVSMPPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMSCCL	420	
Db	361 KRSRSVFYRLTILYLIVFAVSMPPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMSCCL	420	Qy	431 NPILYGLFLNGIQDRL 446	436	
Qy	431 NPILYGLFLNGIQDRL 446	436	Db	421 NPILYGLFLNGIKADL 436	436	
Db	421 NPILYGLFLNGIKADL 436	436	<b>RESULT 4</b>			
	NY5R CANFA	STANDARD;	PRT:	446 AA.		
	ID _NY5R_CANFA					
	AC 06279;					
	DT 15-DIC-1998 (Rel. 37, Created)					
	AC 15-DIC-1998 (Rel. 37, Last sequence update)					
	DT 25-OCT-2004 (Rel. 45, Last annotation update)					
	DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (YS receptor) (NPY5).					
	GN Name=NPY5R; Synonyms=NPY5;					
	OS Canis familiaris (Dog).					
	RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Carnivora; Fissipedia; Canidae; Canis.					
	OC NCBI_TaxID=9615;					
	RN [1] _SEQUENCE FROM N.A.					
	RP RX MEDLINE=98017379; PubMed=9802393; DOI=10.1016/S0167-0115(98)00052-4;					
	RA Borovsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M., Vaysse P., Branchek T.A., Gerald C.; RT "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs".					
	RT Regul. Pept. 75:45-53 (1998).					
	CC -1- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyl cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).					
	CC -1- SUBCELLULAR LOCATION: Integral membrane protein.					
	CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.					
	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).					
	CC DR GO: GO:0016021; C:integral to membrane; IEA.					
	DR GO: GO:004983; F:neuropeptide Y receptor activity; IEA.					
	DR GO: GO:0004872; F:receptor activity; IEA.					
	DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.					
	DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.					
	DR Pfam: PF00001; tcm:1; 1.					
	DR PRINTS: PR00237; GPCR_RHODOPSIN.					
	DR PRINTS: PR01016; NRPEPTIDEYSR.					
	DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.					
	KW Receptor.					
	SQ SEQUENCE 446 AA; 50936 MW; 2C3384B0:90AA:693 CRC64;					
	Query Match Score 83.6%; Best Local Similarity 95.4%; Matches 416; Conservative 9; Mismatches 11; Indels 0; Gaps . 0;					
Db	1 MDLELDIYNTKLTATENNAAATRNSDPPVWDDYKSSYDLDQYFLGLTYFVSLLGFMGNL 70					
	1 MDLELDIYNTKLTATENNAAATRNSDPPVWDDYKSSYDLDQYFLGLTYFVSLLGFMGNL 60					
Qy	71 LILMALMKRNQKTTYNFLIGNLAFSDILVLFCSPEPLTSVLLDWMGRKMCHIMPF 130					
Db	61 LILMALIKRNQKTTYNFLIGNLAFSDILVLFCSPEPLTSVLLDWMGRKMCHIMPF 120					
	1 LILMALIKRNQKTTYNFLIGNLAFSDILVLFCSPEPLTSVLLDWMGRKMCHIMPF 120					
Qy	191 VEQETRGSAUSSRYLVCESWPSDYSRDIATFISLILVQTLPLVCLTVSHTSVCRSISC 250					
Db	181 VEQETFGSAUSSRYLVCESWPSDYSRDIATFISLILVQTLPLVCLTVSHTSVCRSISC 240					
	181 VEQETFGSAUSSRYLVCESWPSDYSRDIATFISLILVQTLPLVCLTVSHTSVCRSISC 240					
Qy	251 GLSNKENRLEENEMINLTHPSKKGSPQVKLGSHKWSYSFIKCKRHSYRKTACTLPAP 310					
Db	241 GLSNKENRLEENEMINLTHPSKKGSPQVKLGSHKWSYSFIKCKRHSYRKTACTLPAP 300					
	241 GLSNKENRLEENEMINLTHPSKKGSPQVKLGSHKWSYSFIKCKRHSYRKTACTLPAP 300					
Qy	311 ERPSQENHRSLPENFGSVRSQLSSSSKKFIPGVPCTFEIKPEENSVDYELRKRSVTRIK 370					
Db	301 ARPSLENQSRTLPNFGSVRSQLSSSSKKFIPGVPCTFEIKPEENSVDYELRKRSVTRIK 360					





Db	301	SFTKRERRYSKTTACTVLPAPGSPQEKKHLYT-PEPGGSTRSQQLSPSSKVTPGVPICFEV	359	FT DOMAIN	179	210	Extracellular (Potential).
Qy	350	KPEENSDVHELRVKRSRSTRIKRSRSYFYLTLIVAFSWMPLHLFHVVTFDNDLNLIS	409	FT TRANSMEM	211	232	5 (Potential).
Db	360	KPEESSDAQEVKRSRSLTRIKRSRSYFYLTLIVAFSWMPLHLFHVVTFDNDLNLIS	419	FT DOMAIN	233	368	Cytoplasmic (Potential).
Qy	410	NRFHKLVYCICHLGMSCCINPILYGFNLNGIORDLQ	447	FT TRANSMEM	369	391	6 (Potential).
Db	420	NRFHKLVYCICHLGMSCCINPILYGFNLNGIADLR	457	FT DOMAIN	392	404	Extracellular (Potential).
				FT TRANSMEM	405	428	7 (Potential).
				FT DOMAIN	429	446	Cytoplasmic (Potential).
				FT CARBOHYD	10	10	N-linked (GlcNAc. . .) (Potential).
				FT CARBOHYD	17	17	N-linked (GlcNAc. . .) (Potential).
				FT DISULFID	114	198	By similarity.
				FT LIPID	442	442	S-palmitoyl cysteine (Potential).
SQ	SEQUENCE	446 AA:	50474 MW;	B7F61_6C2394C6CA0 CRCE4;			
				Query Match	75.5%	Score 1976;	DB 1; Length 446;
				Best Local Similarity	85.1%	Pred. No. 5e-14;	
				Matches 371; Conservative 33; Mismatches 32;		Indels 0; Gaps 0;	
QY	11	MDELDDEYNNKTLEATNTTAATNTSDIFWDDYKSSYDDQFLQFLGLYTFVSLIGFMGNL	70	Db 1 MGSEPIPDYNNKTLEASNNNTVAATNSGE PVWEDYKGSSYDDQFLQFLGLYTFVSLIGFMGNL	60		
QY	71	LILMLAMKRNQKTTVNFLIGNIAFLSTLIVLFCSPFPLTSVLLDQMFGRKTMCHIMPF	130	Db 61 LILMAVMRKRNQKTTVNFLIGNIAFLSTLIVLFCSPFPLTSVLLDQMFGRKTMCHIMPF	120		
QY	131	QCYSVLVSTLILLISIAVRYHMKHPISNNLTANHGFLYLIATWTLGFAICSPLPVPHSL	190	Db 121 QCVTVLVLILISIAVRYHMKHPISNNLTANHGFLYLIATWTLGFAICSPLPVPHSL	180		
QY	191	VELOETFGSALLSSRYLCVESWPSDSYRAFTISLILLYQYLPLVCLTVSHTSVTSVRSISC	250	Db 181 VELQESFGSAWLSRYLCVESWPSDSYRAFTISLILLYQYLPLVCLTVSHTSVTSVRSISC	240		
QY	251	GLSNKENLEENMINLTLPSSKGSGQVKSUGSHWSYSFKRHRYSKTTACTVLPAP	310	Db 241 GLSSQDSKLEENENMINLTQPAKRGSGQAKLSSHPKMTYSFIRRHRYSKTTACTVLPAP	300		
QY	311	ERPSQENHSRILPENFGSVRSOLSSSKFIPGVPCTFEIKPENSVHLYRKRYSKTRIK	370	Db 301 AGPALESBEGRPKGKCSMGSOPPPSKMPGVPTCEVKPENSVPVRSSIMRLR	360		
QY	371	KRSRSVFYRLTILYFAVSMPLHLFHVVTDFDNDLISNRHFKLVYCICHLLGMMSCL	430	Db 361 KRSRSVFYRLTILYFAVSMPLHLFHVVTDFDNDLISNRHFKLVYCICHLLGMMSCL	420		
				RESULT 8			
				OBQFM2			
				ID OBQFM2			
				AC OBQFM2;			
				DT 01-JUN-2002	(TRNMBLrel.	21; Created)	
				DT 01-JUN-2002	(TRNMBLrel.	21; Last annotation update)	
				DT 01-JUN-2003	(TRNMBLrel.	24; Last annotation update)	
				DE Neuropeptide Y receptor Y5.			
				OS Gallus gallus (Chicken).			
				OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
				OX Gallus.			
				NCBI_TaxID-9031;			
				RN [1]			
				SEQUENCE FROM N.A.			
				RA Holmberg S.K.S., Mikko S., Boswell T., Larhammar D.;			
				RT "Pharmacological characterization of cloned chicken neuropeptide Y receptors Y1 and Y5".			
				J. Neurochem. 0-0-0 (2003).			
				RL EMBL; AY04844; AAKG3556.1; -.			
				DR EMBL; GO-0016021; C:integral to membrane; IEA.			
				DR GO; GO-0004983; P:neuropeptide Y receptor activity; IEA.			
				DR GO; GO-0004872; F:receptor activity; IEA.			



PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1;	AC O02813;	DR DT 15-JUL-1998 (Rel. 36, Created)
DR PS00262; G PROTEIN RECEPTOR_F1_2;	DR DT 15-DEC-1998 (Rel. 37, Last sequence update)	
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;	DR DT 25-OCT-2004 (Rel. 45, Last annotation update)	
KW Phosphorylation; Polymorphism; Transmembrane.	DE Neuropeptide Y receptor type 1 (NPY-R).	
DOMAIN 1 39 Extracellular (Potential).	GN Name=NPY1R;	
FT DOMAIN 40 62 Cytoplasmic (Potential).	OS Canis familiaris (Dog).	
FT DOMAIN 63 72 2 (Potential).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
FT TRANSMEM 73 94 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	NCBI_TaxID=9615;	
FT DOMAIN 95 114 Extracellular (Potential).	OX	
FT TRANSMEM 115 136 3 (Potential).	RN	
FT DOMAIN 137 156 Cytoplasmic (Potential).	RP SEQUENCE FROM N.A.	
FT TRANSMEM 157 177 4 (Potential).	RX MEDLINE=99017380; PubMed=9802394; DOI=10.1016/S0167-0115(98)00053-6;	
FT DOMAIN 178 210 Extracellular (Potential).	RA Malmstrom R.E.; Hoekfelt T.; Bjoeriman J.-A.; Nilnen C.; Bystrom M., [1]	
FT TRANSMEM 211 232 5 (Potential).	RA Ekstrand A.J.; Lundberg J.M.; Regul. Pept. 75:55-70(1998).	
FT CARBOHYD 233 263 Cytoplasmic (Potential).	CC FUNCTION: Receptor for neuropeptide Y and peptide YY.	
FT TRANSMEM 264 286 6 (Potential).	CC -!- SUBCELLULAR LOCATION: Integral membrane protein.	
FT DOMAIN 287 299 Extracellular (Potential).	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
FT TRANSMEM 300 323 7 (Potential).	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
FT DOMAIN 324 384 Cytoplasmic (Potential).	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
FT CARBOHYD 2 2 N-linked (GlcNAc. . .) (Potential).	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
FT CARBOHYD 11 11 N-linked (GlcNAc. . .) (Potential).	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
FT CARBOHYD 17 17 N-linked (GlcNAc. . .) (Potential).	CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
FT DISULFID 113 198 By similarity.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration	
FT LIPID 338 338 S-palmitoyl cysteine (Potential).	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
FT VARIANT 374 374 K-> T (In dbSNP:5578) .	CC the European Bioinformatics Institute. There are no restrictions on its	
FT CONFLICT 96 96 /FTid=VAR_014681.	CC use by non-profit institutions at long as its content is in no way	
SEQUENCE 384 AA; 44392 MW; 582B0DB04490316 CRC64;	CC modified and this statement is not removed. Usage by and for commercial	
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	CC or send an email to <a href="mailto:licenses@isb-sib.ch">licenses@isb-sib.ch</a> ).	
• Query Match 29.5%; Score 771.5; DB 1; Length 384;	CC	
Best Local Similarity 34.7%; Pred. No. 1.3e-43;	DR AF005778; AAC08046.1;	
Matches 170; Conservative 75; Mismatches 128; Indels 117; Gaps 8;	DR InterPro; IPR000276; GPCR_Rhodopsin.	
Qy 20 NKTL--ATENNTA---ATPNNSDFPVWDYKSYDDLQFLQLGL--YTFSVLLGPFGNLLI 72	DR InterPro; IPR000511; NPY_Receptor.	
Db 2 NSTLFSQVENHSHVSNSFSKNAOALLAFENDNDCHPLAMIFTALAYGAVITLGYSGNLLA 61	DR PRINTS; PR002337; GPCRRAHODOPSN.	
Qy 73 LMALMKKRQKRTTNYFLIGNGNLAFLSDIILVYLFCSPFTLTSVLDDOMFGKVMCHIMPFLC 132	DR PROSITE; PS002337; G PROTEIN RECEPTOR_F-1; 1.	
Db 62 IIIIKQEMRNVNINLIVLNLSFDLVAIMCLPTFVYLMDEHWVGEAMCKLNPKFYQC 121	DR PROSITE; PS002337; G PROTEIN RECEPTOR_F-2; 1.	
Qy 133 VSVLVSTLILLISIAIVRYMIKHPISNNLTAHGYFLIATWVTLGFAICSPLPVFHSLYE 192	KW G-protein coupled receptor; Glycoprotein; Lipoprotein;	
Db 122 VSITVSISSLVIAVERHOLIINPRGWRPNRNRHAYGIVIWL--AVASSLPLIXQM 179	KW Phosphorylation; Transmembrane.	
Qy 193 LOETPGSALLS--RYYLCVESPWPSDYSYRAFTSLIILQYIILVCLTVSHTSVCRSIS 249	FT DOMAIN 1 39 Extracellular (Potential).	
Db 180 TDEPFQNTVLDKXYCPDQFSPDSHRLSYTTLVLYQFGPCLFCITCYFKI---- 234	FT DOMAIN 2 71 Extracellular (Potential).	
Qy 250 CGLSNKENLLENMNLTHPSKGSQVKLSSGHWSYSFIKKHRRYSKKTACVLEA 309	FT DOMAIN 3 93 Extracellular (Potential).	
Db 235 -----YINLKRR----- 241	FT DOMAIN 4 113 Extracellular (Potential).	
Qy 310 PERPSQENHNSRILPENFGSRSQQLSSSKF1PQGVPTCFEIKPEENSDVHELVRKSVTI 369	FT DOMAIN 5 135 Extracellular (Potential).	
Db 242 -----NMMDKMRDNKYRSSB 257	FT DOMAIN 6 155 Extracellular (Potential).	
Qy 370 KKRSRSVYFLTILVFLWPSWMPHLFLHVYTDFDNLNSRHEFLVYCTCHLJGMMSCC 429	FT DOMAIN 7 176 Extracellular (Potential).	
Db 258 TKR--INNMLSLIVTAAVFLCWLPTTIFNTVFDWNRHQIATCNHLLFLICHUTAMISTIC 314	FT DOMAIN 8 209 Extracellular (Potential).	
Qy 430 LNPILYGFNLNGIQRDLQFFNECDFRSRDDYETIAMSTMHTDVSKTSIKQASPVAFKK 489	FT DOMAIN 9 231 Extracellular (Potential).	
Db 315 VNPIYGFNLKNFNRDQLQFFNECDFRSRDDYETIAMSTMHTDVSKTSIKQASPVAFKK 374	FT DOMAIN 10 262 Extracellular (Potential).	
Qy 490 INNNDNEKI 499	FT DOMAIN 11 285 Extracellular (Potential).	
Db 375 INNNDNEKI 384	FT DOMAIN 12 296 Extracellular (Potential).	
Qy	Query Match 29.1%; Score '761'; DB 1; Length 382;	
Best Local Similarity 35.4%; Pred. No. 6.3e-43;	Best Local Similarity 35.4%; Pred. No. 6.3e-43;	
Matches 167; Conservatives 69; Mismatches 124; Indexes 112; Gaps 7;	Matches 167; Conservatives 69; Mismatches 124; Indexes 112; Gaps 7;	
Qy 32 TRNSDPFWYDDYKSSVDDLQYFLQFLGL--YTFVSLIGFMGNLILMALMKGKRNQKTTVNFLI 90	Db 19 SENSNQFLAEESDDHPLMLPMLAYCAVILIGVNLMLIQLKEMANVNLTILI 78	
Db	Qy 91 GNLAFSDILVVLFCSPFLTSVLDQMFQGKVMCHIMPFLQCVSVLSTLILISTAVRY 150	
RESULT 10		
NY1R_CANFA		
ID_NY1R_CANFA		
STANDARD;	PRT; 382 AA.	



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CC EMBL; ZI1504; CAA77579.1; -.

CC PIR; S12863; S12863.

CC RGD; 3198; NPY1r.

CC InterPro; IPR000276; GPCR\_Rhodopsin.

CC InterPro; IPR000351; NPY1\_receptor.

CC InterPro; IPR000611; NPY\_receptor.

CC Pfam; PF00001; 7tm\_1; 1.

CC PRINTS; PR00237; GPROTEIN\_RECCEP\_F1\_1;

CC PROSITE; PS00237; G\_PROTEIN\_RECCEP\_F1\_2; 1.

CC PROSITE; PS50262; G\_protein\_recceptor; RECCEP\_F1\_2; 1.

CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;

CC KW Phosphorylation; Transmembrane.

CC PT DOMAIN 1 38 Extracellular (Potential).

CC PT TRANSMEM 39 61 1 (Potential).

CC PT DOMAIN 62 71 Cytoplasmic (Potential).

CC PT TRANSMEM 72 93 2 (Potential).

CC PT DOMAIN 94 113 Extracellular (Potential).

CC PT TRANSMEM 114 135 3 (Potential).

CC PT DOMAIN 136 155 Cytoplasmic (Potential).

CC PT TRANSMEM 156 176 4 (Potential).

CC PT DOMAIN 177 209 Extracellular (Potential).

CC PT TRANSMEM 210 231 5 (Potential).

CC PT DOMAIN 232 262 Cytoplasmic (Potential).

CC PT TRANSMEM 263 285 6 (Potential).

CC PT DOMAIN 286 298 Extracellular (Potential).

CC PT TRANSMEM 299 322 7 (Potential).

CC PT DOMAIN 323 382 Cytoplasmic (Potential).

CC PT CARBOHYD 2 11 N-linked (GlcNAc . .) (Potential).

CC PT CARBOHYD 11 17 N-linked (GlcNAc . .) (Potential).

CC PT DISULFID 17 197 N-linked (GlcNAc . .) (Potential).

CC PT DISULFID 112 197 By similarity.

CC PT LIPID 337 337 S-palmitoyl cysteine (Potential).

CC SQ SEQUENCE 382 AA; 44116 MW; 1DEAA038065C07C3 CRC64;

Query Match 28.3%; score 740.5; DB 1; Length 382;

Best Local Similarity 33.6%; Pred. No. 1.5e-41;

Matches 166; Conservative 74; Mismatches 127; Gaps 10;

Qy 20 NKTL--ATENNTA--ATRNSDFPYWDDYKSSVDPDQLQFLGYLTTF----VSILGFNG 68

Db 2 NSTLFRVENVTHNVNSNSPFLAFEN---DCHPLAVIFTLALLAYGAVITLGVSG 56

\* Db 382 AA; 44116 MW; 1DEAA038065C07C3 CRC64;

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Qy 69 NLLLMALMKRNQKTTVNLIGNIAESDILIVLFCSPFLTTSVLDOMMEGKVNCHIMP 128

Db 57 NLALLILILIQKEMRNVTNLIVLNFSIDLIVMCLPFFVYTLMHDHVEGETMCKLNP 116

Qy 129 FLQCYSVLVSTLILISIAVRYHMKHPINNLANTHGFLIATWTGLFAICSPPLPVFH 188

Db 117 FVQCYSITVSIFSLVIAVPERPHQLINPRGRMPNNRHAGTYITVWLAVALSPFPVY 176

Qy 189 SLVELOQETFGSALLSS--RYLCLVESWPSDSYRIATISLILVQYTLPLVCLTVSHTSYC 245

Db 177 ILTD--EPFQTVSLAFLPKTVCFDKPSDHSRLSTYTLILVQYFGPLCPIFICYFKI- 233

Qy 246 RSISCCSLNSKENRLEEMINLTHPSKSKGSPQVKLSGSKHWSSEFIKHRRYSKTKAC 305

Db 234 ----- YTRLKRANNMDK---- 246

Qy 3.06 VLPAPERPSQENHSRILPENFGSVRSQLSSSKF1BGPVTCPEIKPEENSDVHELRVRS 365

Qy 247 ----- IDSKYRSE----- 256

Db 366 VTRIKRSRSVYRLTILVAVSFYMLPHLHVVTDFNDNLISNRHFKVYCICHLSM 425

Db 257 -----TKRINVMILLSIIVAVFAVCMLPLTFTNTYFDWNHIOIATCNHNFLFLICHTAM 309

Qy 4.26 MSCCLNPILGFGLNNGIQRDLQFFNFCDPFSRSRDDYYETIAMSTMHTDVSKTSLKQASPV 485

Db 310 ISTCVNPIFYGPNKFQNDLQFFNFCDPFSRSRDDYYETIAMSTMHTDVSKTSLKQASPV 369

Qy 486 AFKKINNNDDNEKI 499

370 ARKKINNN-DNEKI 382

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Db RESULT 13 NY1R\_PIG STANDARD; PRT; 383 AA.

DR NY1R\_PIG STANDARD; PRT; 383 AA.

DR AC 002835; ID 15-JUL-1998 (Rel. 36, Created)

DR DT 15-JUL-1999 (Rel. 38, Last sequence update)

DR DT 25-OCT-2004 (Rel. 45, Last annotation update)

DR DE Neuropetide Y receptor type 1 (NPY..-R).

DR Name=NPY1R;

DR Sub scrofa (Pig).

DR Mammalia; Butcheria; Cetartiodactyla Suina; Suidae; Subs.

DR NCBI\_TAXID=9823;

DR SEQUENCE FROM N.A.

DR TISSUE-HYPOTHALAMUS; RX PubMed=99017380; DOI=10.1016/S0167-0115(98)00053-6;

DR Malmstrom R.B., Hoekfelt T., Bjoerklund J.-A., Nilnen C., Byström M., Ekstrand A.J., Lundberg J.M.;

DR "Characterization and molecular cloning of vascular neuropeptide Y receptor subtypes in pig and dog.";

DR Regul. Pept. 75:55-70(1998).

DR 121

DR SEQUENCE FROM N.A.

DR Wraith A., Tortenstien A., Chardon P., Harbitz I., Chowdhary B.P., RA

DR Andersson L., Larhammar D.; RT "Porcine NPY receptors NPY1R, NPY2R and NPY5R: cloning, mapping and comparative analysis";

DR Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.

DR -1-FUNCTION; Receptor for neuropeptide Y and peptide YY.

DR -1-SUBCELLULAR LOCATION: Integral membrane protein.

DR -1-SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

DR CC

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DR or send an email to license@isb-sib.ch).

DR CC

DR EMBL; AP005779; AAC26836.1; -.

DR EMBL; AP106081; AAD13776.2; -.

DR InterPro; IPR000276; GPCR\_Rhodopsin.

DR InterPro; IPR000351; NPY1 receptor.

DR InterPro; IPR000611; NPY\_Receptor.

DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR000277; GPCR2HDOPEN.

DR PROSITE; PS000237; G-PROTEIN RECEPTOR\_F1\_1; 1.

DR PROSITE; PS50362; G-PROTEIN RECEPTOR\_F1\_2; 1.

DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;

DR G-protein; Transmembrane.

DR DOMAIN 1 39 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 63 72 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 73 94 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 95 114 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 115 136 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 137 156 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 157 177 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 211 232 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 233 263 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 264 286 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 300 323 Extracellular (Potential).

DR DR Cytoplasmic (Potential).

DR DOMAIN 324 383 N-linked (GlcNAc . .) (Potential).

DR DR N-linked (GlcNAc . .) (Potential).

DR DOMAIN 325 111 N-linked (GlcNAc . .) (Potential).

DR DR N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 17 17 N-linked (GlcNAc. . .) (Potential).  
 FT DISULFID 113 198 By similarity.  
 FT LIPID 338 338 S-palmitoyl cysteine (Potential).

FT CONFLICT 203 203 L > P (in Ref. 2).  
 SQ SEQUENCE 383 AA; 44327 MW; 0D58CB5A549BE62CF CRG64;

Query Match Score 740; DB 1; Length 383;  
 Best Local Similarity 34.1%; Pred. No. 1.6e-41;  
 Matches 167; Conservative 79; Mismatches 126; Gaps 9;

Qy 20 NKTLAT--ENNTA---ATRNSDFPVDYKSSVDDLQFLIGL-YTFVSLGLGMNLII 72  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 2 NSTLSSQVNTHSYTNNSEKNSQFLAFENDDCHPLAMIFTALAGAVIILGVSGNLAL 61

Qy 73 LMALMKGKRNQKITVNFLIGNLAFAFSIDLIVVLFCSPTFLTISVLLDQWMMFGKVNCHIMPFQLC 132  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 62 IIIILKQKEMRVNTNLLVNLNSFSDLVIAIMCLPFFTVYTLMDHWTGEVMCKLNPFVQC 121

Qy 133 VSVLVSTLISIAVRYHMKHPISINNLANTAHGYFLIATWTLGPAICSPLPVFHSVLVE 192  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 122 VSITVSISPLVLTAVERHQLINPRGRPSRNHAAYGAVIWLV--AVASSPLFLYQVL 179

Qy 193 LOETEGSALLSS--RYLCVBSWPSDSYRIAFTISLLQVYLPLVCLTVSHTSVCRSIS 249  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 180 TDBPFPONTVLDAFKDKYVCFCDFKPLSDSHRLSYTTLJLVLQFEGPLCPFICYFKI --- 234

Qy 250 CGLSNKRNENRLEENMINLTLLHSKKSKSPQVKLUSGSHKWSYSSTKHKRRYBRKTACVLPKA 309  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 235 -----YIRLKR----- 241

Qy 310 PERSQENHSRILPENFGSVRSQSLSSSSKF1PGVPTCFEIKPEENSVDHELRVKRSVTI 369  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 242 -----NNNMKDNRDNKYRSSSE 257

Qy 370 KKRSRSSVYRFLTILLYPAVSMPLHLFHVYTDENDNLISNRHFKELYCICHLLGMMSCC 429  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 258 TKR---INVMLLISIVVAFAVCWLPLIINTVDFWNHQIATCNHNULFLICHTAMISTC 314

Qy 430 LNPIIYGFLANNIQDLOFFNFCDPDRSRDDYYETIAMSTWHTDVSKTSLKQASPVAFRK 489  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 315 INPIFYGLNKNQFDLQFFFNFCDFRSRDDYYEVITAMSMTWHTDVSKTSLKQASPVALKK 374

Qy 490 INNDNONEKI 499  
 :||:||:||:||:||:  
 Db 375 I-HSDNONEKI 383

RESULT 14  
 ID NY1R MOUSE STANDARD; PRT; 382 AA.  
 AC Q04573; Q81993;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 25-Oct-2004 (Rel. 45, Last annotation update)  
 DE Neurotrophin Y receptor type 1 (NPY1-R).  
 GN Name-Npy1r;  
 OS Mus musculus (Mouse).  
 OC Mectzoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10050;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=9310619; PubMed=1468559; DOI=10.1016/0014-5793(92)81490-D;  
 RA Eva C., Oberto A., Spranghel R., Genazzani E., "The murine NPY-1 receptor gene. Structure and delineation of tissue-specific expression"; FEBS Lett. 314:285-288 (1992).  
 RN [2] SEQUENCE FROM N.A.  
 RX MEDLINE=96102072; PubMed=8530415; DOI=10.1074/jbc.270.50.30102;  
 RA Nakamura M., Sakanaoka C., Aoki Y., Ogasawara H., Tsuji T., Kodama H., Matsumoto T., Shimizu T., Noma M.,

RT "Identification of two isoforms of mouse neuropeptide Y-Y1 receptor generated by alternative splicing. Isolation, genomic structure, and functional expression of the receptors.".  
 RT J. Biol. Chem. 270:30102-30110(1995).  
 RL -!  
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=NPY1-R alpha;  
 CC IsoID=Q04573;1; Sequence=Displayed;  
 CC Name=NPY1-R beta;  
 CC IsoID=Q04573-2; Sequence=VP 001912; VSP 001913;  
 CC -!- TISSUE SPECIFICITY: The alpha Form is highly expressed in the brain, heart, kidney, spleen, skeletal muscle, and lung, whereas the beta receptor mRNA was not detected in these tissues. However, the beta form is expressed in mouse embryonic developmental stage (7 and 11 days), bone marrow cells and several hematopoietic cell lines.  
 CC -!- DEVELOPMENTAL STAGE: The beta form is expressed in embryonic development stage (7 and 11 days). The beta form is an embryonic and a bone marrow form of NPY1-R, which decreases in the expression during development and differentiation.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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 CC -!- DR EMBL; Z1BZ80; CAA79157.1; --;  
 CC DR EMBL; Z1BZ81; -: NOT\_ANNOTATED\_CDS.  
 CC DR EMBL; D63818; BAA09387.1; --;  
 CC DR EMBL; S2738B; S2738B; BAA09388.1; --;  
 CC DR PIR:S2738B; S2738B;  
 CC DR MGD; MGI:104963; Npyp1r.  
 CC DR GO; GO:0001602; F:pancreatic polypeptide receptor activity; IDA.  
 CC DR GO; GO:0001601; F:peptide YY receptor activity; IDA.  
 CC DR GO; GO:0007631; P:feeding behavior; IMP.  
 CC DR GO; GO:0006006; P:glucose metabolism; IMP.  
 CC DR GO; GO:0007626; P:locomotor behavior; IMP.  
 CC DR GO; GO:0019233; P:perception of pain; IMP.  
 CC DR GO; GO:0008217; P:regulation of blood pressure; IMP.  
 CC DR GO; GO:000014; P:regulation of body size; IMP.  
 CC DR InterPro; IPR000076; GPCR\_Rhodopsin.  
 CC DR InterPro; IPR0000351; NPY1\_receptor.  
 CC DR InterPro; IPR0000611; NPY1\_Receptor.  
 CC DR PFAM; PF00001; 7cm1; 1  
 CC DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 CC DR PROSITE; PS00237; G\_PROB1 RECEP\_F1\_1;  
 CC DR PROSITE; PS5082; G\_PROTEIN\_RECEP\_F1\_2;  
 CC KW Alternative splicing; G\_protein\_coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane; DOMAIN 1 38 Extracellular (Potential).  
 CC PT TRANSMEM 39 61 1 (Potential).  
 CC PT DOMAIN 62 71 Cytoplasmic (Potential).  
 CC PT TRANSMEM 72 93 2 (Potential).  
 CC PT DOMAIN 94 113 Extracellular (Potential).  
 CC PT TRANSMEM 114 135 3 (Potential).  
 CC PT DOMAIN 136 155 Cytoplasmic (Potential).  
 CC PT TRANSMEM 156 176 4 (Potential).  
 CC PT DOMAIN 177 209 Extracellular (Potential).  
 CC PT TRANSMEM 210 231 5 (Potential).  
 CC PT DOMAIN 232 262 Cytoplasmic (Potential).  
 CC PT TRANSMEM 263 285 6 (Potential).  
 CC PT DOMAIN 286 298 Extracellular (Potential).  
 CC PT TRANSMEM 299 322 7 (Potential).  
 CC PT DOMAIN 323 382 Cytoplasmic (Potential).  
 CC PT CARBOHYD 2 2 N-linked (GlcNAc. . .) (Potential).  
 CC PT CARBOHYD 11 11 N-linked (GlcNAc. . .) (Potential).  
 CC PT CARBOHYD 17 17 N-linked (GlcNAc. . .) (Potential).



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Qy	413	FKLVYCICHLLGMMSCCUNPILYGLNGIORDLOPFFNFCDFRSRDDYETIAMSTMHT	472
	298	HNLLFLICHLPTAMISTCVNPITYGLNKNGDLOPFFNFCDFRSRDDYETIAMSTMHT	357
Db			
Qy	473	DYSKTSLKQASPVAFKKINNNDDNEKI	499
	358	DYSKTSLKQASPLAFKKI-SCVENEKI	383
Db			

Search completed: June 7, 2005, 17:58:44  
Job time : 182 secs

